

# SUBSTITUTE SEQUENCE LISTING

<110> Bihain, Bernard  
Bougueleret, Lydie  
Yen-Potin, Frances

<120> LSR Receptor, Its Activity, Its Cloning and Its Application To  
The Diagnosis Prevention And/or Treatment of Obesity and  
Related Risks or Complications

<130> GENSET.035APC

<150> FR 97/10088  
<151> 1997-08-06

<150> FR 98/05032  
<151> 1998-04-22

<160> 41

<170> Patent.pm

<210> 1  
<211> 2097  
<212> DNA  
<213> Rattus norvegicus

<400> 1  
accgctcacc aggtcagttg tccccggaaa gccgaaggca tgagcttcgc ccaagttctt 60  
tttatggggtt agaactcctc cagagcgggg gaaaaaggac ttggaatagg ggcgggacgg 120  
agcacgcacc cttctccgcc ttggttctcg ccgcgcccc tactctcggg atacttggga 180  
ggggacgcgc gggcaccgtc gctgctagac ggccgcg atg gcg ccg gcg gcc ggc 235  
Met Ala Pro Ala Ala Gly  
1 5  
gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg 283  
Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val  
10 15 20  
tgt ctc ttt ctc atc att ttc tgc cca gac cct gcc agt gcc atc cag 331  
Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp Pro Ala Ser Ala Ile Gln  
25 30 35  
gtg act gtg tct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg 379  
Val Thr Val Ser Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val  
40 45 50  
acc ctg ccc tgc acc tat cag atg agc aac act ctc aca gtc ccc atc 427  
Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Val Pro Ile  
55 60 65 70  
gtg atc tgg aag tac aag tca ttc tgc cgg gac cgt att gcc gat gcc 475

Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	Arg	Asp	Arg	Ile	Ala	Asp	Ala		
				75					80					85			
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct		523
Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu	Asn	Ala	Gln	Leu	Ala	Ala		
			90					95					100				
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc		571
Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu	Cys	Gln	Asp	Ser	Val	Arg		
		105					110					115					
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga		619
Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly	Asn	Ala	Val	Thr	Leu	Gly		
	120					125					130						
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg		667
Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Asp	Leu		
135					140					145					150		
acc	ttc	gag	cag	aca	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tct		715
Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser		
				155					160					165			
gtg	gtc	tcg	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag		763
Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Tyr	Ala	Glu		
			170					175					180				
ctc	atc	gtc	ctt	ggc	agg	acc	tca	gag	gcc	cct	gag	ctc	cta	cct	ggt		811
Leu	Ile	Val	Leu	Gly	Arg	Thr	Ser	Glu	Ala	Pro	Glu	Leu	Leu	Pro	Gly		
		185					190					195					
ttt	cgg	gcg	ggg	ccc	ttg	gaa	gat	tgg	ctc	ttt	gtg	gtc	gtg	gtc	tgc		859
Phe	Arg	Ala	Gly	Pro	Leu	Glu	Asp	Trp	Leu	Phe	Val	Val	Val	Val	Cys		
	200					205					210						
ctg	gcg	agc	ctc	ctc	ctc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag		907
Leu	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Gly	Ile	Cys	Trp	Cys	Gln		
215					220					225					230		
tgc	tgt	cct	cac	acc	tgc	tgc	tgc	tat	gtc	cga	tgt	ccc	tgc	tgc	cca		955
Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro		
				235				240					245				
gac	aag	tgc	tgt	tgc	cct	gag	gct	ctt	tat	gct	gct	ggc	aaa	gca	gcc		1003
Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala		
				250				255					260				
acc	tca	ggt	gtc	ccg	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc		1051
Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	His	Leu		
		265					270					275					
tca	cct	gcc	aag	acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc		1099
Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	Met	Gly		
	280					285					290						
cct	ccc	tat	ggg	tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggt		1147
Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	Ser	Val	Gly		

295		300		305		310	
ggc cac agc tcc caa gta ccc ctg ctg cgt gac gtg gat ggc agt gta	Gly His Ser Ser Gln Val Pro Leu Leu Arg Asp Val Asp Gly Ser Val	1195					
	315 320 325						
tct tca gaa gta cga agt ggc tac agg atc cag gct aac cag caa gat	Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp	1243					
	330 335 340						
gac tcc atg agg gtc cta tac tat atg gag aaa gag cta gcc aac ttt	Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe	1291					
	345 350 355						
gac cct tcc cga cct ggc cct ccc aat ggc aga gtg gaa cgg gcc atg	Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu Arg Ala Met	1339					
	360 365 370						
agt gaa gta acc tcc ctc cat gaa gat gac tgg cga tcg agg cct tcc	Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser	1387					
	375 380 385 390						
agg gct cct gcc ctc acc ccc atc agg gat gag gag tgg aat cgc cac	Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn Arg His	1435					
	395 400 405						
tcc cca cag agt ccc aga aca tgg gag cag gaa ccc ctt caa gaa caa	Ser Pro Gln Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln	1483					
	410 415 420						
cca agg ggt ggt tgg ggg tct gga cgc cct cgg gcc cgc tct gtg gat	Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser Val Asp	1531					
	425 430 435						
gct cta gat gat atc aac cgg cct ggc tcc act gaa tca gga cgg tct	Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser	1579					
	440 445 450						
tct ccc cca agt agt gga cgg aga gga cgg gcc tat gca cct cca aga	Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg	1627					
	455 460 465 470						
agt cgc agc cgg gat gac ctc tat gac ccg gac gat cct agg gac ttg	Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu	1675					
	475 480 485						
cca cat tcc cga gat ccc cac tat tat gac gac atc agg tct aga gat	Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Ile Arg Ser Arg Asp	1723					
	490 495 500						
cca cgt gct gac ccc aga tcc cgt cag cga tcc cga gat cct cgg gat	Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser Arg Asp Pro Arg Asp	1771					
	505 510 515						
gct ggc ttc agg tca agg gac cct cag tat gat ggg cga cta tta gaa	Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu	1819					
	520 525 530						

gag gct tta aag aaa aag ggg tcg ggc gag aga agg agg gtt tac agg 1867  
 Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu Arg Arg Arg Val Tyr Arg  
 535 540 545 550  
  
 gag gaa gaa gag gaa gag gag ggc caa tac ccc cca gca cct cca cct 1915  
 Glu Glu Glu Glu Glu Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro  
 555 560 565  
  
 tac tca gag act gac tcg cag gcc tca cgg gag agg agg ctg aaa aag 1963  
 Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys  
 570 575 580  
  
 aat ttg gcc ctg agt cgg gaa agt tta gtc gtc tga tccacgtttt 2009  
 Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val \*  
 585 590  
  
 gtatgtagct tttgtacttt ttttttaatt ggaatcaata ttgatgaaac ttcaagccta 2069  
  
 ataaaatgtc taatcacaaa aaaaaaaaaa 2097

<210> 2  
 <211> 593  
 <212> PRT  
 <213> Rattus norvegicus

<400> 2  
 Met Ala Pro Ala Ala Gly Ala Cys Ala Gly Ala Pro Asp Ser His Pro  
 1 5 10 15  
  
 Ala Thr Val Val Phe Val Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp  
 20 25 30  
  
 Pro Ala Ser Ala Ile Gln Val Thr Val Ser Asp Pro Tyr His Val Val  
 35 40 45  
  
 Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn  
 50 55 60  
  
 Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg  
 65 70 75 80  
  
 Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu  
 85 90 95  
  
 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu  
 100 105 110  
  
 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly  
 115 120 125  
  
 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile  
 130 135 140  
  
 Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser

145					150					155				160
Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly
				165					170					175
Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Gly	Arg	Thr	Ser	Glu
			180					185					190	Ala
Pro	Glu	Leu	Leu	Pro	Gly	Phe	Arg	Ala	Gly	Pro	Leu	Glu	Asp	Trp
		195					200					205		Leu
Phe	Val	Val	Val	Val	Cys	Leu	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu
	210					215					220			
Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr
225					230					235				240
Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu
				245					250					255
Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala
			260					265					270	Pro
Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro
		275					280					285		
Ala	Met	Ile	Pro	Met	Gly	Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe
	290					295					300			Asp
Arg	His	Ser	Ser	Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu
305					310					315				320
Asp	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg
				325					330					335
Gln	Ala	Asn	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met
			340					345					350	Glu
Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn
		355					360					365		Gly
Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp
	370					375					380			Asp
Trp	Arg	Ser	Arg	Pro	Ser	Arg	Ala	Pro	Ala	Leu	Thr	Pro	Ile	Arg
385					390					395				400
Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Gln	Ser	Pro	Arg	Thr	Trp	Glu
			405						410					415
Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly	Ser	Gly	Arg
			420					425					430	Pro
Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn	Arg	Pro	Gly
		435					440					445		Ser
Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly	Arg	Arg	Gly
														Arg

450		455		460
Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro				
465		470		480
Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp				
	485		490	495
Asp Ile Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg				
	500		505	510
Ser Arg Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr				
	515		520	525
Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu				
	530		535	540
Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu Gly Gln Tyr				
545		550		560
Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg				
	565		570	575
Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val				
	580		585	590

Val

<210> 3  
 <211> 2040  
 <212> DNA  
 <213> Rattus norvegicus

<400> 3	
accgctcacc aggtcagttg tccccggaaa gccgaaggca tgagcttcgc ccaagttctt	60
tttatggggtt agaactcctc cagagcgggg gaaaaaggac ttggaatagg ggcgggacgg	120
agcacgcacc cttctccgcc ttggttctcg ccgcgcccc tactctcggg atacttggga	180
ggggacgcgc gggcaccgtc gctgctagac ggccgcg atg gcg ccg gcg gcc ggc	235
	Met Ala Pro Ala Ala Gly
	1 5
gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg	283
Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val	
	10 15 20
tgt ctc ttt ctc atc att ttc tgc cca gac cct gcc agt gcc atc cag	331
Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp Pro Ala Ser Ala Ile Gln	
	25 30 35
gtg act gtg tct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg	379
Val Thr Val Ser Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val	
	40 45 50
acc ctg ccc tgc acc tat cag atg agc aac act ctc aca gtc ccc atc	427

Thr 55	Leu	Pro	Cys	Thr 60	Tyr	Gln	Met	Ser	Asn 65	Thr	Leu	Thr	Val	Pro	Ile 70	
gtg	atc	tgg	aag	tac	aag	tca	ttc	tgc	cgg	gac	cgt	att	gcc	gat	gcc	475
Val	Ile	Trp	Lys	Tyr 75	Lys	Ser	Phe	Cys	Arg 80	Asp	Arg	Ile	Ala	Asp	Ala 85	
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct	523
Phe	Ser	Pro	Ala 90	Ser	Val	Asp	Asn	Gln 95	Leu	Asn	Ala	Gln	Leu 100	Ala	Ala	
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc	571
Gly	Asn	Pro 105	Gly	Tyr	Asn	Pro	Tyr 110	Val	Glu	Cys	Gln	Asp 115	Ser	Val	Arg	
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga	619
Thr	Val 120	Arg	Val	Val	Ala	Thr 125	Lys	Gln	Gly	Asn	Ala 130	Val	Thr	Leu	Gly	
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667
Asp	Tyr	Tyr	Gln	Gly	Arg 140	Arg	Ile	Thr	Ile	Thr 145	Gly	Asn	Ala	Asp	Leu 150	
acc	ttc	gag	cag	aca	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tct	715
Thr	Phe	Glu	Gln	Thr 155	Ala	Trp	Gly	Asp 160	Ser	Gly	Val	Tyr	Tyr	Cys 165	Ser	
gtg	gtc	tgc	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag	763
Val	Val	Ser	Ala 170	Gln	Asp	Leu	Asp 175	Gly	Asn	Asn	Glu	Ala	Tyr 180	Ala	Glu	
ctc	atc	gtc	ctt	gat	tgg	ctc	ttt	gtg	gtc	gtg	gtc	tgc	ctg	gcg	agc	811
Leu	Ile	Val 185	Leu	Asp	Trp	Leu	Phe 190	Val	Val	Val	Val	Cys 195	Leu	Ala	Ser	
ctc	ctc	ctc	ttc	ctc	ctc	ctg	ggc	atc	tgc	tgg	tgc	cag	tgc	tgt	cct	859
Leu	Leu	Leu	Phe	Leu	Leu	Leu 205	Gly	Ile	Cys	Trp	Cys 210	Gln	Cys	Cys	Pro	
cac	acc	tgc	tgc	tgc	tat	gtc	cga	tgt	ccc	tgc	tgc	cca	gac	aag	tgc	907
His	Thr	Cys	Cys	Cys	Tyr 220	Val	Arg	Cys	Pro	Cys 225	Cys	Pro	Asp	Lys	Cys 230	
tgt	tgc	cct	gag	gct	ctt	tat	gct	gct	ggc	aaa	gca	gcc	acc	tca	ggt	955
Cys	Cys	Pro	Glu	Ala 235	Leu	Tyr	Ala	Ala	Gly 240	Lys	Ala	Ala	Thr 245	Ser	Gly	
gtc	ccg	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc	tca	cct	gcc	1003
Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser 255	Ile	Tyr	Thr	His	Leu	Ser 260	Pro	Ala	
aag	acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc	cct	ccc	tat	1051
Lys	Thr	Pro 265	Pro	Pro	Pro	Pro	Ala 270	Met	Ile	Pro	Met	Gly 275	Pro	Pro	Tyr	
ggg	tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggt	ggc	cac	agc	1099
Gly	Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	Ser	Val	Gly	Gly	His	Ser	



280	285	290	
tcc caa gta ccc ctg ctg cgt gac gtg gat ggc agt gta tct tca gaa Ser Gln Val Pro Leu Leu Arg Asp Val Asp Gly Ser Val Ser Ser Glu 295 300 305 310			1147
gta cga agt ggc tac agg atc cag gct aac cag caa gat gac tcc atg Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met 315 320 325			1195
agg gtc cta tac tat atg gag aaa gag cta gcc aac ttt gac cct tcc Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser 330 335 340			1243
cga cct ggc cct ccc aat ggc aga gtg gaa cgg gcc atg agt gaa gta Arg Pro Gly Pro Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val 345 350 355			1291
acc tcc ctc cat gaa gat gac tgg cga tcg agg cct tcc agg gct cct Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro 360 365 370			1339
gcc ctc acc ccc atc agg gat gag gag tgg aat cgc cac tcc cca cag Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Gln 375 380 385 390			1387
agt ccc aga aca tgg gag cag gaa ccc ctt caa gaa caa cca agg ggt Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly 395 400 405			1435
ggt tgg ggg tct gga cgc cct cgg gcc cgc tct gtg gat gct cta gat Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp 410 415 420			1483
gat atc aac cgg cct ggc tcc act gaa tca gga cgg tct tct ccc cca Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro 425 430 435			1531
agt agt gga cgg aga gga cgg gcc tat gca cct cca aga agt cgc agc Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser 440 445 450			1579
cgg gat gac ctc tat gac ccg gac gat cct agg gac ttg cca cat tcc Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser 455 460 465 470			1627
cga gat ccc cac tat tat gac gac atc agg tct aga gat cca cgt gct Arg Asp Pro His Tyr Tyr Asp Asp Ile Arg Ser Arg Asp Pro Arg Ala 475 480 485			1675
gac ccc aga tcc cgt cag cga tcc cga gat cct cgg gat gct ggc ttc Asp Pro Arg Ser Arg Gln Arg Ser Arg Asp Pro Arg Asp Ala Gly Phe 490 495 500			1723
agg tca agg gac cct cag tat gat ggg cga cta tta gaa gag gct tta Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu 505 510 515			1771



aag aaa aag ggg tcg ggc gag aga agg agg gtt tac agg gag gaa gaa 1819  
 Lys Lys Lys Gly Ser Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu  
 520 525 530

gag gaa gag gag ggc caa tac ccc cca gca cct cca cct tac tca gag 1867  
 Glu Glu Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu  
 535 540 545 550

act gac tcg cag gcc tca cgg gag agg agg ctg aaa aag aat ttg gcc 1915  
 Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala  
 555 560 565

ctg agt cgg gaa agt tta gtc gtc tga tccacgtttt gtatgtagct 1962  
 Leu Ser Arg Glu Ser Leu Val Val \*  
 570

tttgtacttt ttttttaatt ggaatcaata ttgatgaaac ttcaagccta ataaaatgtc 2022

taatcacaaa aaaaaaaaaa 2040

<210> 4  
 <211> 574  
 <212> PRT  
 <213> Rattus norvegicus

<400> 4  
 Met Ala Pro Ala Ala Gly Ala Cys Ala Gly Ala Pro Asp Ser His Pro  
 1 5 10 15  
 Ala Thr Val Val Phe Val Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp  
 20 25 30  
 Pro Ala Ser Ala Ile Gln Val Thr Val Ser Asp Pro Tyr His Val Val  
 35 40 45  
 Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn  
 50 55 60  
 Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg  
 65 70 75 80  
 Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu  
 85 90 95  
 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu  
 100 105 110  
 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly  
 115 120 125  
 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile  
 130 135 140  
 Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser  
 145 150 155 160

Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn  
 165 170 175  
 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp Trp Leu Phe Val Val  
 180 185 190  
 Val Val Cys Leu Ala Ser Leu Leu Leu Phe Leu Leu Leu Gly Ile Cys  
 195 200 205  
 Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val Arg Cys Pro  
 210 215 220  
 Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu Tyr Ala Ala Gly  
 225 230 235 240  
 Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr  
 245 250 255  
 Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro Ala Met Ile  
 260 265 270  
 Pro Met Gly Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg His Ser  
 275 280 285  
 Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg Asp Val Asp  
 290 295 300  
 Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn  
 305 310 315 320  
 Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu  
 325 330 335  
 Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu  
 340 345 350  
 Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser  
 355 360 365  
 Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp  
 370 375 380  
 Asn Arg His Ser Pro Gln Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu  
 385 390 395 400  
 Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg  
 405 410 415  
 Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser  
 420 425 430  
 Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala  
 435 440 445  
 Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro  
 450 455 460

Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Ile Arg  
 465 470 475 480  
 Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser Arg Asp  
 485 490 495  
 Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg  
 500 505 510  
 Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ser Gly Glu Arg Arg Arg  
 515 520 525  
 Val Tyr Arg Glu Glu Glu Glu Glu Glu Gly Gln Tyr Pro Pro Ala  
 530 535 540  
 Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg  
 545 550 555 560  
 Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val  
 565 570

<210> 5  
 <211> 1893  
 <212> DNA  
 <213> Rattus norvegicus

<400> 5  
 accgctcacc aggtcagttg tccccggaaa gccgaaggca tgagcttcgc ccaagttctt 60  
 tttatggggtt agaactcctc cagagcgggg gaaaaaggac ttggaatagg ggcgggacgg 120  
 agcacgcacc cttctccgcc ttggttctcg ccgcgcccc tactctcggg atacttggga 180  
 ggggacgcgc gggcaccgtc gctgctagac ggccgcg atg gcg ccg gcg gcc ggc 235  
 Met Ala Pro Ala Ala Gly  
 1 5  
 gcg tgt gct ggg gcg cct gac tcc cac cca gct acc gtg gtc ttc gtg 283  
 Ala Cys Ala Gly Ala Pro Asp Ser His Pro Ala Thr Val Val Phe Val  
 10 15 20  
 tgt ctc ttt ctc atc att ttc tgc cca gac cct gcc agt gcc atc cag 331  
 Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp Pro Ala Ser Ala Ile Gln  
 25 30 35  
 gtg act gtg tct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg 379  
 Val Thr Val Ser Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val  
 40 45 50  
 acc ctg ccc tgc acc tat cag atg agc aac act ctc aca gtc ccc atc 427  
 Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Val Pro Ile  
 55 60 65 70  
 gtg atc tgg aag tac aag tca ttc tgc cgg gac cgt att gcc gat gcc 475  
 Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala

75										80					85					
ttc	tct	cct	gcc	agt	gtg	gac	aac	cag	cta	aat	gcc	cag	ttg	gca	gct	523				
Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	Leu	Asn	Ala	Gln	Leu	Ala	Ala					
			90					95					100							
ggc	aac	ccc	ggc	tac	aac	ccc	tat	gtg	gag	tgc	cag	gac	agt	gta	cgc	571				
Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	Glu	Cys	Gln	Asp	Ser	Val	Arg					
		105					110					115								
act	gtc	agg	gtg	gtg	gcc	acc	aaa	cag	ggc	aat	gcg	gtg	acc	ctg	gga	619				
Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly	Asn	Ala	Val	Thr	Leu	Gly					
	120					125					130									
gac	tac	tac	caa	ggc	agg	agg	atc	acc	ata	aca	gga	aat	gct	gac	ctg	667				
Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile	Thr	Gly	Asn	Ala	Asp	Leu					
135					140					145					150					
acc	ttc	gag	cag	aca	gcc	tgg	gga	gac	agt	gga	gtg	tat	tac	tgc	tct	715				
Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser	Gly	Val	Tyr	Tyr	Cys	Ser					
				155					160					165						
gtg	gtc	tcg	gcc	caa	gat	ctg	gat	gga	aac	aac	gag	gcg	tac	gca	gag	763				
Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Tyr	Ala	Glu					
			170					175					180							
ctc	atc	gtc	ctt	gtt	tat	gct	gct	ggc	aaa	gca	gcc	acc	tca	ggt	gtc	811				
Leu	Ile	Val	Leu	Val	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val					
		185					190					195								
ccg	agc	atc	tat	gcc	ccc	agc	atc	tat	acc	cac	ctc	tca	cct	gcc	aag	859				
Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	Lys					
	200					205					210									
acc	cca	cca	cct	ccg	cct	gcc	atg	att	ccc	atg	ggc	cct	ccc	tat	ggg	907				
Thr	Pro	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	Met	Gly	Pro	Pro	Tyr	Gly					
215					220					225					230					
tac	cct	gga	gac	ttt	gac	aga	cat	agc	tca	gtt	ggt	ggc	cac	agc	tcc	955				
Tyr	Pro	Gly	Asp	Phe	Asp	Arg	His	Ser	Ser	Val	Gly	Gly	His	Ser	Ser					
				235					240					245						
caa	gta	ccc	ctg	ctg	cgt	gac	gtg	gat	ggc	agt	gta	tct	tca	gaa	gta	1003				
Gln	Val	Pro	Leu	Leu	Arg	Asp	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	Val					
			250					255					260							
cga	agt	ggc	tac	agg	atc	cag	gct	aac	cag	caa	gat	gac	tcc	atg	agg	1051				
Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn	Gln	Gln	Asp	Asp	Ser	Met	Arg					
		265					270					275								
gtc	cta	tac	tat	atg	gag	aaa	gag	cta	gcc	aac	ttt	gac	cct	tcc	cga	1099				
Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg					
	280					285					290									
cct	ggc	cct	ccc	aat	ggc	aga	gtg	gaa	cgg	gcc	atg	agt	gaa	gta	acc	1147				
Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr					
295					300					305					310					

tcc ctc cat gaa gat gac tgg cga tcg agg cct tcc agg gct cct gcc	1195
Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala	
315 320 325	
ctc acc ccc atc agg gat gag gag tgg aat cgc cac tcc cca cag agt	1243
Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Gln Ser	
330 335 340	
ccc aga aca tgg gag cag gaa ccc ctt caa gaa caa cca agg ggt ggt	1291
Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly	
345 350 355	
tgg ggg tct gga cgc cct cgg gcc cgc tct gtg gat gct cta gat gat	1339
Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp	
360 365 370	
atc aac cgg cct ggc tcc act gaa tca gga cgg tct tct ccc cca agt	1387
Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser	
375 380 385 390	
agt gga cgg aga gga cgg gcc tat gca cct cca aga agt cgc agc cgg	1435
Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg	
395 400 405	
gat gac ctc tat gac ccg gac gat cct agg gac ttg cca cat tcc cga	1483
Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser Arg	
410 415 420	
gat ccc cac tat tat gac gac atc agg tct aga gat cca cgt gct gac	1531
Asp Pro His Tyr Tyr Asp Asp Ile Arg Ser Arg Asp Pro Arg Ala Asp	
425 430 435	
ccc aga tcc cgt cag cga tcc cga gat cct cgg gat gct ggc ttc agg	1579
Pro Arg Ser Arg Gln Arg Ser Arg Asp Pro Arg Asp Ala Gly Phe Arg	
440 445 450	
tca agg gac cct cag tat gat ggg cga cta tta gaa gag gct tta aag	1627
Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys	
455 460 465 470	
aaa aag ggg tcg ggc gag aga agg agg gtt tac agg gag gaa gaa gag	1675
Lys Lys Gly Ser Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu	
475 480 485	
gaa gag gag ggc caa tac ccc cca gca cct cca cct tac tca gag act	1723
Glu Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr	
490 495 500	
gac tcg cag gcc tca cgg gag agg agg ctg aaa aag aat ttg gcc ctg	1771
Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu	
505 510 515	
agt cgg gaa agt tta gtc gtc tga tccacgtttt gtatgtagct tttgtacttt	1825
Ser Arg Glu Ser Leu Val Val *	

520

525

ttttttaatt ggaatcaata ttgatgaaac ttcaagccta ataaaatgtc taatcacaaa 1885

aaaaaaaaa 1893

&lt;210&gt; 6

&lt;211&gt; 525

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 6

Met Ala Pro Ala Ala Gly Ala Cys Ala Gly Ala Pro Asp Ser His Pro  
1 5 10 15

Ala Thr Val Val Phe Val Cys Leu Phe Leu Ile Ile Phe Cys Pro Asp  
20 25 30

Pro Ala Ser Ala Ile Gln Val Thr Val Ser Asp Pro Tyr His Val Val  
35 40 45

Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Ser Asn  
50 55 60

Thr Leu Thr Val Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg  
65 70 75 80

Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu  
85 90 95

Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu  
100 105 110

Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly  
115 120 125

Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile  
130 135 140

Thr Gly Asn Ala Asp Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser  
145 150 155 160

Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn  
165 170 175

Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Val Tyr Ala Ala Gly Lys  
180 185 190

Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr Thr  
195 200 205

His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro Ala Met Ile Pro  
210 215 220

Met Gly Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg His Ser Ser

225					230					235				240
Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu	Arg	Asp	Val	Asp Gly
				245					250					255
Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Asn Gln
			260					265					270	
Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu Ala
		275					280					285		
Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu Arg
	290					295					300			
Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser Arg
305					310					315				320
Pro	Ser	Arg	Ala	Pro	Ala	Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp Asn
				325					330					335
Arg	His	Ser	Pro	Gln	Ser	Pro	Arg	Thr	Trp	Glu	Gln	Glu	Pro	Leu Gln
			340					345					350	
Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly	Ser	Gly	Arg	Pro	Arg	Ala	Arg Ser
		355					360					365		
Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn	Arg	Pro	Gly	Ser	Thr	Glu	Ser Gly
	370					375					380			
Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly	Arg	Arg	Gly	Arg	Ala	Tyr	Ala Pro
385					390					395				400
Pro	Arg	Ser	Arg	Ser	Arg	Asp	Asp	Leu	Tyr	Asp	Pro	Asp	Asp	Pro Arg
				405					410					415
Asp	Leu	Pro	His	Ser	Arg	Asp	Pro	His	Tyr	Tyr	Asp	Asp	Ile	Arg Ser
			420					425					430	
Arg	Asp	Pro	Arg	Ala	Asp	Pro	Arg	Ser	Arg	Gln	Arg	Ser	Arg	Asp Pro
		435					440					445		
Arg	Asp	Ala	Gly	Phe	Arg	Ser	Arg	Asp	Pro	Gln	Tyr	Asp	Gly	Arg Leu
	450					455					460			
Leu	Glu	Glu	Ala	Leu	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Arg	Arg	Arg Val
465					470					475				480
Tyr	Arg	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Gln	Tyr	Pro	Pro	Ala Pro
				485					490					495
Pro	Pro	Tyr	Ser	Glu	Thr	Asp	Ser	Gln	Ala	Ser	Arg	Glu	Arg	Arg Leu
			500					505					510	
Lys	Lys	Asn	Leu	Ala	Leu	Ser	Arg	Glu	Ser	Leu	Val	Val		
		515					520					525		



<210> 7  
 <211> 2158  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> Misc\_Feature  
 <222> 1259..1261  
 <223> Potential splicing site AAG

<221> Misc\_Feature  
 <222> 1657  
 <223> Potential insertion of a AGG

<400> 7  
 tggagtgtgg ctcgaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc 60  
 atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac 115  
 Met Gln Gln Asp  
 1  
 gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg 163  
 Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val  
 5 10 15 20  
 cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga 211  
 His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly  
 25 30 35  
 agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg 259  
 Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala Met Ala Leu Leu  
 40 45 50  
 gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc 307  
 Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly  
 55 60 65  
 cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca 355  
 Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr  
 70 75 80  
 gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg 403  
 Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val  
 85 90 95 100  
 gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc 451  
 Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Thr  
 105 110 115  
 tcg acc ccc acg caa ccc atc gtc atc tgg aag tac aag tct ttc tgc 499  
 Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys  
 120 125 130

egg gac cgc atc gcc gat gcc ttc tcc ccg gcc agc gtc gac aac cag	547
Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln	
135 140 145	
ctc aat gcc cag ctg gca gcc ggg aac cca ggc tac aac ccc tac gtt	595
Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val	
150 155 160	
gag tgc cag gac agc gtg cgc acc gtc agg gtc gtg gcc acc aag cag	643
Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln	
165 170 175 180	
ggc aac gct gtg acc ctg gga gat tac tac cag ggc cgg agg att acc	691
Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr	
185 190 195	
atc acc gga aat gct gac ctg acc ttt gac cag acg gcg tgg ggg gac	739
Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr Ala Trp Gly Asp	
200 205 210	
agt ggt gtg tat tac tgc tcc gtg gtc tca gcc cag gac ctc cag ggg	787
Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Gln Gly	
215 220 225	
aac aat gag gcc tac gca gag ctc atc gtc ctt ggg agg acc tca ggg	835
Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly Arg Thr Ser Gly	
230 235 240	
gtg gct gag ctc tta cct ggt ttt cag gcg ggg ccc ata gaa gac tgg	883
Val Ala Glu Leu Leu Pro Gly Phe Gln Ala Gly Pro Ile Glu Asp Trp	
245 250 255 260	
ctc ttc gtg gtt gtg gta tgc ctg gct gcc ttc ctc atc ttc ctc ctc	931
Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu Leu	
265 270 275	
ctg ggc atc tgc tgg tgc cag tgc tgc ccg cac act tgc tgc tgc tac	979
Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr	
280 285 290	
gtc agg tgc ccc tgc tgc cca gac aag tgc tgc tgc ccc gag gcc ctg	1027
Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu	
295 300 305	
tat gcc gcc ggc aaa gca gcc acc tca ggt gtt ccc agc att tat gcc	1075
Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala	
310 315 320	
ccc agc acc tat gcc cac ctg tct ccc gcc aag acc cca ccc cca cca	1123
Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro	
325 330 335 340	
gct atg att ccc atg ggc cct gcc tac aac ggg tac cct gga gga tac	1171
Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly Tyr	
345 350 355	
cct gga gac gtt gac agg agt agc tca gct ggt ggc caa ggc tcc tat	1219

Pro	Gly	Asp	Val	Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser	Tyr	
			360						365							370
gta	ccc	ctg	ctt	cgg	gac	acg	gac	agc	agt	gtg	gcc	tct	gaa	gtc	cgc	1267
Val	Pro	Leu	Leu	Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val	Arg	
		375					380					385				
agt	ggc	tac	agg	att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	1315
Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	
	390					395					400					
ctg	tac	tac	atg	gag	aag	gag	ctg	gcc	aac	ttc	gac	cct	tct	cga	cct	1363
Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	
405					410					415					420	
ggc	ccc	ccc	agt	ggc	cgt	gtg	gag	cgg	gcc	atg	agt	gaa	gtc	acc	tcc	1411
Gly	Pro	Pro	Ser	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	
				425					430					435		
ctc	cac	gag	gac	gac	tgg	cga	tct	cgg	cct	tcc	cgg	ggc	cct	gcc	ctc	1459
Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Gly	Pro	Ala	Leu	
			440					445					450			
acc	ccg	atc	cgg	gat	gag	gag	tgg	ggt	ggc	cac	tcc	ccc	cgg	agt	ccc	1507
Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Gly	Gly	His	Ser	Pro	Arg	Ser	Pro	
		455					460					465				
agg	gga	tgg	gac	cag	gag	ccc	gcc	agg	gag	cag	gca	ggc	ggg	ggc	tgg	1555
Arg	Gly	Trp	Asp	Gln	Glu	Pro	Ala	Arg	Glu	Gln	Ala	Gly	Gly	Gly	Trp	
	470					475					480					
cgg	gcc	agg	cgg	ccc	cgg	gcc	cgc	tcc	gtg	gac	gcc	ctg	gac	gac	ctc	1603
Arg	Ala	Arg	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Leu	
485					490					495					500	
acc	ccg	ccg	agc	acc	gcc	gag	tca	ggg	agc	agg	tct	ccc	acg	agt	aat	1651
Thr	Pro	Pro	Ser	Thr	Ala	Glu	Ser	Gly	Ser	Arg	Ser	Pro	Thr	Ser	Asn	
				505					510					515		
ggt	ggg	aga	agc	cgg	gcc	tac	atg	ccc	ccg	cgg	agc	cgc	agc	cgg	gac	1699
Gly	Gly	Arg	Ser	Arg	Ala	Tyr	Met	Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	
			520					525					530			
gac	ctc	tat	gac	caa	gac	gac	tcg	agg	gac	ttc	cca	cgc	tcc	cgg	gac	1747
Asp	Leu	Tyr	Asp	Gln	Asp	Asp	Ser	Arg	Asp	Phe	Pro	Arg	Ser	Arg	Asp	
		535					540					545				
ccc	cac	tac	gac	gac	ttc	agg	tct	cgg	gag	cgc	cct	cct	gcc	gac	ccc	1795
Pro	His	Tyr	Asp	Asp	Phe	Arg	Ser	Arg	Glu	Arg	Pro	Pro	Ala	Asp	Pro	
		550				555					560					
agg	tcc	cac	cac	cac	cgt	acc	cgg	gac	cct	cgg	gac	aac	ggc	tcc	agg	1843
Arg	Ser	His	His	His	Arg	Thr	Arg	Asp	Pro	Arg	Asp	Asn	Gly	Ser	Arg	
565					570					575					580	

tcc ggg gac ctc ccc tat gat ggg cgg cta ctg gag gag gct gtg agg	1891
Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg	
585 590 595	
aag aag ggg tcg gag gag agg agg aga ccc cac aag gag gag gag gaa	1939
Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu	
600 605 610	
gag gcc tac tac ccg ccc gcg ccg ccc ccg tac tcg gag acc gac tcg	1987
Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser	
615 620 625	
cag gcg tcc cga gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg	2035
Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg	
630 635 640	
gaa agt tta gtc gtc tga tctgacgttt tctacgtagc ttttgtatatt	2083
Glu Ser Leu Val Val *	
645	
tttttttttaa tttgaaggaa cactgatgaa gccctgccat acccctcccg agtctaataa	2143
aacgtataat cacaa	2158

<210> 8  
 <211> 649  
 <212> PRT  
 <213> Homo sapiens

<220>

<221> Misc\_Feature  
 <222> 386  
 <223> Potential deletion of a Glu

<221> Misc\_Feature  
 <222> 518  
 <223> Potential insertion of a Arg

<400> 8
Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys
1 5 10 15
Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu
20 25 30
Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala
35 40 45
Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro
50 55 60
Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser
65 70 75 80

Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn  
 85 90 95  
 Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr  
 100 105 110  
 Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr  
 115 120 125  
 Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser  
 130 135 140  
 Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr  
 145 150 155 160  
 Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val  
 165 170 175  
 Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly  
 180 185 190  
 Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr  
 195 200 205  
 Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln  
 210 215 220  
 Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Gly  
 225 230 235 240  
 Arg Thr Ser Gly Val Ala Glu Leu Leu Pro Gly Phe Gln Ala Gly Pro  
 245 250 255  
 Ile Glu Asp Trp Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu  
 260 265 270  
 Ile Phe Leu Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr  
 275 280 285  
 Cys Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys  
 290 295 300  
 Pro Glu Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro  
 305 310 315 320  
 Ser Ile Tyr Ala Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr  
 325 330 335  
 Pro Pro Pro Pro Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr  
 340 345 350  
 Pro Gly Gly Tyr Pro Gly Asp Val Asp Arg Ser Ser Ser Ala Gly Gly  
 355 360 365  
 Gln Gly Ser Tyr Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala  
 370 375 380

Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp  
 385 390 395 400  
 Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp  
 405 410 415  
 Pro Ser Arg Pro Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser  
 420 425 430  
 Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg  
 435 440 445  
 Gly Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser  
 450 455 460  
 Pro Arg Ser Pro Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala  
 465 470 475 480  
 Gly Gly Gly Trp Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala  
 485 490 495  
 Leu Asp Asp Leu Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser  
 500 505 510  
 Pro Thr Ser Asn Gly Gly Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser  
 515 520 525  
 Arg Ser Arg Asp Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro  
 530 535 540  
 Arg Ser Arg Asp Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro  
 545 550 555 560  
 Pro Ala Asp Pro Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp  
 565 570 575  
 Asn Gly Ser Arg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu  
 580 585 590  
 Glu Ala Val Arg Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys  
 595 600 605  
 Glu Glu Glu Glu Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser  
 610 615 620  
 Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu  
 625 630 635 640  
 Ala Leu Ser Arg Glu Ser Leu Val Val  
 645

<210> 9  
 <211> 2101  
 <212> DNA  
 <213> Homo sapiens

<400> 9

tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc	60
atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac	115
	Met Gln Gln Asp
	1
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg	163
Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val	
5 10 15 20	
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga	211
His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly	
25 30 35	
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg	259
Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala Met Ala Leu Leu	
40 45 50	
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc	307
Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly	
55 60 65	
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca	355
Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr	
70 75 80	
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg	403
Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val	
85 90 95 100	
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc	451
Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr Tyr Gln Met Thr	
105 110 115	
tcg acc ccc acg caa ccc atc gtc atc tgg aag tac aag tct ttc tgc	499
Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys	
120 125 130	
cgg gac gcg atc gcc gat gcc ttc tcc ccg gcc agc gtc gac aac cag	547
Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln	
135 140 145	
ctc aat gcc cag ctg gca gcc ggg aac cca ggc tac aac ccc tac gtt	595
Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val	
150 155 160	
gag tgc cag gac agc gtg cgc acc gtc agg gtc gtg gcc acc aag cag	643
Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln	
165 170 175 180	
ggc aac gct gtg acc ctg gga gat tac tac cag ggc cgg agg att acc	691
Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr	
185 190 195	
atc acc gga aat gct gac ctg acc ttt gac cag acg gcg tgg ggg gac	739



Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr Ala Trp Gly Asp	
200 205 210	
agt ggt gtg tat tac tgc tcc gtg gtc tca gcc cag gac ctc cag ggg	787
Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Gln Gly	
215 220 225	
aac aat gag gcc tac gca gag ctc atc gtc ctt gac tgg ctc ttc gtg	835
Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp Trp Leu Phe Val	
230 235 240	
gtt gtg gta tgc ctg gct gcc ttc ctc atc ttc ctc ctc ctg ggc atc	883
Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu Leu Leu Gly Ile	
245 250 255 260	
tgc tgg tgc cag tgc tgc ccg cac act tgc tgc tgc tac gtc agg tgc	931
Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val Arg Cys	
265 270 275	
ccc tgc tgc cca gac aag tgc tgc tgc ccc gag gcc ctg tat gcc gcc	979
Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu Tyr Ala Ala	
280 285 290	
ggc aaa gca gcc acc tca ggt gtt ccc agc att tat gcc ccc agc acc	1027
Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Thr	
295 300 305	
tat gcc cac ctg tct ccc gcc aag acc cca ccc cca cca gct atg att	1075
Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Ala Met Ile	
310 315 320	
ccc atg ggc cct gcc tac aac ggg tac cct gga gga tac cct gga gac	1123
Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly Tyr Pro Gly Asp	
325 330 335 340	
gtt gac agg agt agc tca gct ggt ggc caa ggc tcc tat gta ccc ctg	1171
Val Asp Arg Ser Ser Ser Ala Gly Gly Gln Gly Ser Tyr Val Pro Leu	
345 350 355	
ctt cgg gac acg gac agc agt gtg gcc tct gaa gtc cgc agt ggc tac	1219
Leu Arg Asp Thr Asp Ser Ser Val Ala Ser Glu Val Arg Ser Gly Tyr	
360 365 370	
agg att cag gcc agc cag cag gac gac tcc atg cgg gtc ctg tac tac	1267
Arg Ile Gln Ala Ser Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr	
375 380 385	
atg gag aag gag ctg gcc aac ttc gac cct tct cga cct ggc ccc ccc	1315
Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro	
390 395 400	
agt ggc cgt gtg gag cgg gcc atg agt gaa gtc acc tcc ctc cac gag	1363
Ser Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His Glu	
405 410 415 420	

gac gac tgg cga tct cgg cct tcc cgg ggc cct gcc ctc acc ccg atc Asp Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu Thr Pro Ile 425 430 435	1411
cgg gat gag gag tgg ggt ggc cac tcc ccc cgg agt ccc agg gga tgg Arg Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro Arg Gly Trp 440 445 450	1459
gac cag gag ccc gcc agg gag cag gca ggc ggg ggc tgg cgg gcc agg Asp Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp Arg Ala Arg 455 460 465	1507
cgg ccc cgg gcc cgc tcc gtg gac gcc ctg gac gac ctc acc ccg ccg Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu Thr Pro Pro 470 475 480	1555
agc acc gcc gag tca ggg agc agg tct ccc acg agt aat ggt ggg aga Ser Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn Gly Gly Arg 485 490 495 500	1603
agc cgg gcc tac atg ccc ccg cgg agc cgc agc cgg gac gac ctc tat Ser Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr 505 510 515	1651
gac caa gac gac tcg agg gac ttc cca cgc tcc cgg gac ccc cac tac Asp Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg Asp Pro His Tyr 520 525 530	1699
gac gac ttc agg tct cgg gag cgc cct cct gcc gac ccc agg tcc cac Asp Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp Pro Arg Ser His 535 540 545	1747
cac cac cgt acc cgg gac cct cgg gac aac ggc tcc agg tcc ggg gac His His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser Arg Ser Gly Asp 550 555 560	1795
ctc ccc tat gat ggg cgg cta ctg gag gag gct gtg agg aag aag ggg Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg Lys Lys Gly 565 570 575 580	1843
tcg gag gag agg agg aga ccc cac aag gag gag gag gaa gag gcc tac Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu Glu Ala Tyr 585 590 595	1891
tac ccg ccc gcg ccg ccc ccg tac tcg gag acc gac tcg cag gcg tcc Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser 600 605 610	1939
cga gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg gaa agt tta Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu 615 620 625	1987
gtc gtc tga tctgacgttt tctacgtagc ttttgtattt ttttttttaa Val Val * 630	2036
tttgaaggaa cactgatgaa gccctgccat acccctcccg agtctaataa aacgtataat	2096

cacaa

2101

<210> 10  
<211> 630  
<212> PRT  
<213> Homo sapiens

<400> 10  
Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys  
1 5 10 15  
Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu  
20 25 30  
Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala  
35 40 45  
Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro  
50 55 60  
Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser  
65 70 75 80  
Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn  
85 90 95  
Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr  
100 105 110  
Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr  
115 120 125  
Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser  
130 135 140  
Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr  
145 150 155 160  
Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val  
165 170 175  
Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly  
180 185 190  
Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr  
195 200 205  
Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln  
210 215 220  
Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp  
225 230 235 240  
Trp Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu

245							250							255						
Leu	Leu	Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys					
			260					265					270							
Tyr	Val	Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala					
		275					280					285								
Leu	Tyr	Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr					
	290					295					300									
Ala	Pro	Ser	Thr	Tyr	Ala	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro					
305					310					315					320					
Pro	Ala	Met	Ile	Pro	Met	Gly	Pro	Ala	Tyr	Asn	Gly	Tyr	Pro	Gly	Gly					
			325						330					335						
Tyr	Pro	Gly	Asp	Val	Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser					
		340					345						350							
Tyr	Val	Pro	Leu	Leu	Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val					
	355						360					365								
Arg	Ser	Gly	Tyr	Arg	Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg					
370					375						380									
Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg					
385					390					395					400					
Pro	Gly	Pro	Pro	Ser	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr					
				405					410					415						
Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Gly	Pro	Ala					
		420					425						430							
Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Gly	Gly	His	Ser	Pro	Arg	Ser					
	435					440						445								
Pro	Arg	Gly	Trp	Asp	Gln	Glu	Pro	Ala	Arg	Glu	Gln	Ala	Gly	Gly	Gly					
450					455						460									
Trp	Arg	Ala	Arg	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp					
465					470					475					480					
Leu	Thr	Pro	Pro	Ser	Thr	Ala	Glu	Ser	Gly	Ser	Arg	Ser	Pro	Thr	Ser					
				485					490					495						
Asn	Gly	Gly	Arg	Ser	Arg	Ala	Tyr	Met	Pro	Pro	Arg	Ser	Arg	Ser	Arg					
		500					505						510							
Asp	Asp	Leu	Tyr	Asp	Gln	Asp	Asp	Ser	Arg	Asp	Phe	Pro	Arg	Ser	Arg					
	515					520					525									
Asp	Pro	His	Tyr	Asp	Asp	Phe	Arg	Ser	Arg	Glu	Arg	Pro	Pro	Ala	Asp					
530						535				540										
Pro	Arg	Ser	His	His	His	Arg	Thr	Arg	Asp	Pro	Arg	Asp	Asn	Gly	Ser					

545		550		555		560
Arg Ser Gly Asp	Leu Pro Tyr Asp	Gly Arg	Leu Leu Glu Glu	Ala Val		
	565		570	575		
Arg Lys Lys Gly	Ser Glu Glu Arg	Arg Arg	Pro His Lys	Glu Glu Glu		
	580	585		590		
Glu Glu Ala Tyr	Tyr Pro Pro	Ala Pro Pro	Tyr Ser	Glu Thr Asp		
	595	600	605			
Ser Gln Ala Ser	Arg Glu Arg	Arg Leu Lys	Lys Asn	Leu Ala Leu Ser		
	610	615	620			
Arg Glu Ser Leu	Val Val					
625	630					

<210> 11  
 <211> 1954  
 <212> DNA  
 <213> Homo sapiens

<400> 11

tggagtgtgg ctcggaggac cgcggcgggt caagcacctt tctcccccat atctgaaagc	60
atgccctttg tccacgtcgt ttacgctcat taaaacttcc aga atg caa cag gac	115
	Met Gln Gln Asp
	1
gga ctt gga gta ggg aca agg aac gga agt ggg aag ggg agg agc gtg	163
Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys Gly Arg Ser Val	
5 10 15 20	
cac ccc tcc tgg cct tgg tgc gcg ccg cgc ccc cta agg tac ttt gga	211
His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu Arg Tyr Phe Gly	
25 30 35	
agg gac gcg cgg gcc aga cgc gcc cag acg gcc gcg atg gcg ctg ttg	259
Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala Met Ala Leu Leu	
40 45 50	
gcc ggc ggg ctc tcc aga ggg ctg ggc tcc cac ccg gcc gcc gca ggc	307
Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro Ala Ala Ala Gly	
55 60 65	
cgg gac gcg gtc gtc ttc gtg tgg ctt ctg ctt agc acc tgg tgc aca	355
Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser Thr Trp Cys Thr	
70 75 80	
gct cct gcc agg gcc atc cag gtg acc gtg tcc aac ccc tac cac gtg	403
Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn Pro Tyr His Val	
85 90 95 100	
gtg atc ctc ttc cag cct gtg acc ctg ccc tgt acc tac cag atg acc	451

Val	Ile	Leu	Phe	Gln	Pro	Val	Thr	Leu	Pro	Cys	Thr	Tyr	Gln	Met	Thr	
				105					110					115		
tcg	acc	ccc	acg	caa	ccc	atc	gtc	atc	tgg	aag	tac	aag	tct	ttc	tgc	499
Ser	Thr	Pro	Thr	Gln	Pro	Ile	Val	Ile	Trp	Lys	Tyr	Lys	Ser	Phe	Cys	
			120					125					130			
cgg	gac	cgc	atc	gcc	gat	gcc	ttc	tcc	ccg	gcc	agc	gtc	gac	aac	cag	547
Arg	Asp	Arg	Ile	Ala	Asp	Ala	Phe	Ser	Pro	Ala	Ser	Val	Asp	Asn	Gln	
		135					140					145				
ctc	aat	gcc	cag	ctg	gca	gcc	ggg	aac	cca	ggc	tac	aac	ccc	tac	gtt	595
Leu	Asn	Ala	Gln	Leu	Ala	Ala	Gly	Asn	Pro	Gly	Tyr	Asn	Pro	Tyr	Val	
	150					155					160					
gag	tgc	cag	gac	agc	gtg	cgc	acc	gtc	agg	gtc	gtg	gcc	acc	aag	cag	643
Glu	Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	
165					170				175						180	
ggc	aac	gct	gtg	acc	ctg	gga	gat	tac	tac	cag	ggc	cgg	agg	att	acc	691
Gly	Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	
				185				190						195		
atc	acc	gga	aat	gct	gac	ctg	acc	ttt	gac	cag	acg	gcg	tgg	ggg	gac	739
Ile	Thr	Gly	Asn	Ala	Asp	Leu	Thr	Phe	Asp	Gln	Thr	Ala	Trp	Gly	Asp	
			200					205					210			
agt	ggt	gtg	tat	tac	tgc	tcc	gtg	gtc	tca	gcc	cag	gac	ctc	cag	ggg	787
Ser	Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Gln	Gly	
		215					220					225				
aac	aat	gag	gcc	tac	gca	gag	ctc	atc	gtc	ctt	gtg	tat	gcc	gcc	ggc	835
Asn	Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Val	Tyr	Ala	Ala	Gly	
	230					235					240					
aaa	gca	gcc	acc	tca	ggt	gtt	ccc	agc	att	tat	gcc	ccc	agc	acc	tat	883
Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro	Ser	Thr	Tyr	
245					250				255						260	
gcc	cac	ctg	tct	ccc	gcc	aag	acc	cca	ccc	cca	cca	gct	atg	att	ccc	931
Ala	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Ala	Met	Ile	Pro	
				265				270						275		
atg	ggc	cct	gcc	tac	aac	ggg	tac	cct	gga	gga	tac	cct	gga	gac	gtt	979
Met	Gly	Pro	Ala	Tyr	Asn	Gly	Tyr	Pro	Gly	Gly	Tyr	Pro	Gly	Asp	Val	
			280					285					290			
gac	agg	agt	agc	tca	gct	ggt	ggc	caa	ggc	tcc	tat	gta	ccc	ctg	ctt	1027
Asp	Arg	Ser	Ser	Ser	Ala	Gly	Gly	Gln	Gly	Ser	Tyr	Val	Pro	Leu	Leu	
		295					300					305				
cgg	gac	acg	gac	agc	agt	gtg	gcc	tct	gaa	gtc	cgc	agt	ggc	tac	agg	1075
Arg	Asp	Thr	Asp	Ser	Ser	Val	Ala	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	
	310					315					320					
att	cag	gcc	agc	cag	cag	gac	gac	tcc	atg	cgg	gtc	ctg	tac	tac	atg	1123
Ile	Gln	Ala	Ser	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	

325	330	335	340	
gag aag gag ctg gcc aac ttc gac cct tct cga cct ggc ccc ccc agt				1171
Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Ser	345	350	355	
ggc cgt gtg gag cgg gcc atg agt gaa gtc acc tcc ctc cac gag gac				1219
Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp	360	365	370	
gac tgg cga tct cgg cct tcc cgg ggc cct gcc ctc acc ccg atc cgg				1267
Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu Thr Pro Ile Arg	375	380	385	
gat gag gag tgg ggt ggc cac tcc ccc cgg agt ccc agg gga tgg gac				1315
Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro Arg Gly Trp Asp	390	395	400	
cag gag ccc gcc agg gag cag gca ggc ggg ggc tgg cgg gcc agg cgg				1363
Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp Arg Ala Arg Arg	405	410	415	420
ccc cgg gcc cgc tcc gtg gac gcc ctg gac gac ctc acc ccg ccg agc				1411
Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu Thr Pro Pro Ser	425	430	435	
acc gcc gag tca ggg agc agg tct ccc acg agt aat ggt ggg aga agc				1459
Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn Gly Gly Arg Ser	440	445	450	
cgg gcc tac atg ccc ccg cgg agc cgc agc cgg gac gac ctc tat gac				1507
Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp	455	460	465	
caa gac gac tcg agg gac ttc cca cgc tcc cgg gac ccc cac tac gac				1555
Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg Asp Pro His Tyr Asp	470	475	480	
gac ttc agg tct cgg gag cgc cct cct gcc gac ccc agg tcc cac cac				1603
Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp Pro Arg Ser His His	485	490	495	500
cac cgt acc cgg gac cct cgg gac aac ggc tcc agg tcc ggg gac ctc				1651
His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser Arg Ser Gly Asp Leu	505	510	515	
ccc tat gat ggg cgg cta ctg gag gag gct gtg agg aag aag ggg tcg				1699
Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg Lys Lys Gly Ser	520	525	530	
gag gag agg agg aga ccc cac aag gag gag gag gaa gag gcc tac tac				1747
Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu Glu Ala Tyr Tyr	535	540	545	
ccg ccc gcg ccg ccc ccg tac tcg gag acc gac tcg cag gcg tcc cga				1795
Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg	550	555	560	



gag cgc agg ctc aag aag aac ttg gcc ctg agt cgg gaa agt tta gtc 1843  
 Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val  
 565 570 575 580

gtc tga tctgacgttt tctacgtagc ttttgtatatt ttttttttaa tttgaaggaa 1899  
 Val \*

cactgatgaa gccctgccat acccctcccg agtctaataa aacgtataat cacaa 1954

<210> 12  
 <211> 581  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys  
 1 5 10 15  
 Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu  
 20 25 30  
 Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala  
 35 40 45  
 Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro  
 50 55 60  
 Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser  
 65 70 75 80  
 Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn  
 85 90 95  
 Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr  
 100 105 110  
 Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr  
 115 120 125  
 Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser  
 130 135 140  
 Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr  
 145 150 155 160  
 Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val  
 165 170 175  
 Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly  
 180 185 190  
 Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr  
 195 200 205

Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln  
 210 215 220  
 Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Val  
 225 230 235 240  
 Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala  
 245 250 255  
 Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro  
 260 265 270  
 Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly Tyr  
 275 280 285  
 Pro Gly Asp Val Asp Arg Ser Ser Ser Ala Gly Gly Gln Gly Ser Tyr  
 290 295 300  
 Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala Ser Glu Val Arg  
 305 310 315 320  
 Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp Ser Met Arg Val  
 325 330 335  
 Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro  
 340 345 350  
 Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser  
 355 360 365  
 Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu  
 370 375 380  
 Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro  
 385 390 395 400  
 Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp  
 405 410 415  
 Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu  
 420 425 430  
 Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn  
 435 440 445  
 Gly Gly Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg Asp  
 450 455 460  
 Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg Asp  
 465 470 475 480  
 Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp Pro  
 485 490 495  
 Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser Arg  
 500 505 510

Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val Arg  
515 520 525

Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu Glu  
530 535 540

Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser  
545 550 555 560

Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser Arg  
565 570 575

Glu Ser Leu Val Val  
580

<210> 13  
<211> 1886  
<212> DNA  
<213> Mus musculus

<400> 13  
gcaccgtcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct 52  
Met Ala Pro Ala Ala Ser Ala Cys Ala  
1 5

ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt 100  
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe  
10 15 20 25

ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg 148  
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val  
30 35 40

cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac 196  
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His  
45 50 55

tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg 244  
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp  
60 65 70

aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct 292  
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro  
75 80 85

gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc 340  
Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro  
90 95 100 105

ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg 388  
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg  
110 115 120

gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac	436
Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr	
125 130 135	
cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag	484
Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu	
140 145 150	
cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca	532
Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser	
155 160 165	
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc	580
Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val	
170 175 180 185	
ctt ggc agg acc tca gaa gcc cct gag ctc cta cct ggt ttt cgg gcg	628
Leu Gly Arg Thr Ser Glu Ala Pro Glu Leu Leu Pro Gly Phe Arg Ala	
190 195 200	
ggg ccc ttg gaa gat tgg ctc ttt gtg gtc gtg gtc tgc ctg gca agc	676
Gly Pro Leu Glu Asp Trp Leu Phe Val Val Val Val Cys Leu Ala Ser	
205 210 215	
ctc ctc ttc ttc ctc ctc ctg ggc atc tgc tgg tgc cag tgc tgt ccc	724
Leu Leu Phe Phe Leu Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro	
220 225 230	
cac acc tgc tgc tgc tat gtc aga tgt ccc tgc tgc cca gac aag tgc	772
His Thr Cys Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys	
235 240 245	
tgt tgc cct gag gcc ctt tat gct gct ggc aaa gca gcc acc tca ggt	820
Cys Cys Pro Glu Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly	
250 255 260 265	
gtg cca agc atc tat gcc ccc agc atc tat acc cac ctc tct cct gcc	868
Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala	
270 275 280	
aag act ccg cca cct ccg cct gcc atg att ccc atg cgt cct ccc tat	916
Lys Thr Pro Pro Pro Pro Pro Ala Met Ile Pro Met Arg Pro Pro Tyr	
285 290 295	
ggg tac cct gga gac ttt gac agg acc agc tca gtt ggt ggc cac agc	964
Gly Tyr Pro Gly Asp Phe Asp Arg Thr Ser Ser Val Gly Gly His Ser	
300 305 310	
tcc cag gtg ccc ctg ctg cgt gaa gtg gat ggg agc gta tct tca gaa	1012
Ser Gln Val Pro Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu	
315 320 325	
gta cga agt ggc tac agg atc cag gct aac cag caa gat gac tcc atg	1060
Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met	
330 335 340 345	
agg gtc cta tac tat atg gag aag gag cta gcc aac ttc gat cct tcc	1108

Arg	Val	Leu	Tyr	Tyr	Met	Glu	Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser		
				350					355					360			
cgg	cct	ggc	cct	ccc	aat	ggc	cga	gtg	gaa	cgg	gcc	atg	agt	gaa	gta		1156
Arg	Pro	Gly	Pro	Pro	Asn	Gly	Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val		
			365					370					375				
acc	tcc	ctc	cat	gaa	gat	gac	tgg	cga	tct	cgg	cct	tcc	agg	gct	cct		1204
Thr	Ser	Leu	His	Glu	Asp	Asp	Trp	Arg	Ser	Arg	Pro	Ser	Arg	Ala	Pro		
		380					385					390					
gcc	ctc	aca	ccc	atc	agg	gat	gag	gag	tgg	aat	cgc	cac	tcc	cct	cgg		1252
Ala	Leu	Thr	Pro	Ile	Arg	Asp	Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg		
	395					400					405						
agt	ccc	aga	aca	tgg	gag	cag	gaa	ccc	ctt	caa	gaa	cag	cca	agg	ggt		1300
Ser	Pro	Arg	Thr	Trp	Glu	Gln	Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly		
410					415				420						425		
ggt	tgg	ggg	tct	ggg	cgg	cct	cgg	gcc	cgc	tct	gtg	gat	gct	cta	gat		1348
Gly	Trp	Gly	Ser	Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp		
				430				435						440			
gac	atc	aac	cgg	cct	ggc	tcc	act	gaa	tca	gga	agg	tct	tct	ccc	cca		1396
Asp	Ile	Asn	Arg	Pro	Gly	Ser	Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro		
			445					450					455				
agt	agt	gga	cgg	aga	ggg	cgg	gcc	tat	gca	cct	ccg	aga	agt	cgc	agc		1444
Ser	Ser	Gly	Arg	Arg	Gly	Arg	Ala	Tyr	Ala	Pro	Pro	Arg	Ser	Arg	Ser		
		460					465					470					
cgg	gat	gac	ctc	tat	gac	ccc	gac	gat	cct	aga	gac	ttg	cca	cat	tcc		1492
Arg	Asp	Asp	Leu	Tyr	Asp	Pro	Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser		
	475					480					485						
cga	gat	ccc	cac	tat	tat	gat	gat	ttg	agg	tct	agg	gat	cca	cgt	gct		1540
Arg	Asp	Pro	His	Tyr	Tyr	Asp	Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala		
490					495				500						505		
gac	ccc	aga	tcc	cgt	cag	cga	tcc	cac	gat	cct	cgg	gat	gct	ggc	ttc		1588
Asp	Pro	Arg	Ser	Arg	Gln	Arg	Ser	His	Asp	Pro	Arg	Asp	Ala	Gly	Phe		
				510				515						520			
agg	tca	cgg	gac	cct	cag	tat	gat	ggg	cga	ctc	tta	gaa	gag	gct	tta		1636
Arg	Ser	Arg	Asp	Pro	Gln	Tyr	Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu		
			525					530					535				
aag	aaa	aaa	ggg	gct	ggg	gag	aga	aga	cgc	gtt	tac	agg	gag	gaa	gaa		1684
Lys	Lys	Lys	Gly	Ala	Gly	Glu	Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu		
		540					545					550					
gaa	gaa	gaa	gag	gag	ggc	cac	tat	ccc	cca	gca	cct	ccg	cct	tac	tct		1732
Glu	Glu	Glu	Glu	Glu	Gly	His	Tyr	Pro	Pro	Ala	Pro	Pro	Pro	Tyr	Ser		
	555					560					565						
gag	act	gac	tcg	cag	gcc	tcg	agg	gag	cgg	agg	atg	aaa	aag	aat	ttg		1780
Glu	Thr	Asp	Ser	Gln	Ala	Ser	Arg	Glu	Arg	Arg	Met	Lys	Lys	Asn	Leu		

570	575	580	585	
gcc ctg agt cgg gaa agt tta gtc gtc tga tcccacgttt tgttatgtag				1830
Ala Leu Ser Arg Glu Ser Leu Val Val *				
590				
cttttataact tttttaattg gaattattgat gaaactcttc accaagccta ataaaa				1886
<210> 14				
<211> 1829				
<212> DNA				
<213> Mus musculus				
<400> 14				
gcaccgtcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct				52
Met Ala Pro Ala Ala Ser Ala Cys Ala				
1 5				
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt				100
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe				
10 15 20 25				
ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg				148
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val				
30 35 40				
cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac				196
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His				
45 50 55				
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg				244
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp				
60 65 70				
aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct				292
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro				
75 80 85				
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc				340
Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro				
90 95 100 105				
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg				388
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg				
110 115 120				
gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac				436
Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr				
125 130 135				
cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag				484
Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu				
140 145 150				

cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca	532
Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser	
155 160 165	
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc	580
Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val	
170 175 180 185	
ctt gat tgg ctc ttt gtg gtc gtg gtc tgc ctg gca agc ctc ctc ttc	628
Leu Asp Trp Leu Phe Val Val Val Val Cys Leu Ala Ser Leu Leu Phe	
190 195 200	
ttc ctc ctc ctg ggc atc tgc tgg tgc cag tgc tgt ccc cac acc tgc	676
Phe Leu Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys	
205 210 215	
tgc tgc tat gtc aga tgt ccc tgc tgc cca gac aag tgc tgt tgc cct	724
Cys Cys Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro	
220 225 230	
gag gcc ctt tat gct gct ggc aaa gca gcc acc tca ggt gtg cca agc	772
Glu Ala Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser	
235 240 245	
atc tat gcc ccc agc atc tat acc cac ctc tct cct gcc aag act ccg	820
Ile Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro	
250 255 260 265	
cca cct ccg cct gcc atg att ccc atg cgt cct ccc tat ggg tac cct	868
Pro Pro Pro Pro Ala Met Ile Pro Met Arg Pro Pro Tyr Gly Tyr Pro	
270 275 280	
gga gac ttt gac agg acc agc tca gtt ggt ggc cac agc tcc cag gtg	916
Gly Asp Phe Asp Arg Thr Ser Ser Val Gly Gly His Ser Ser Gln Val	
285 290 295	
ccc ctg ctg cgt gaa gtg gat ggg agc gta tct tca gaa gta cga agt	964
Pro Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser	
300 305 310	
ggc tac agg atc cag gct aac cag caa gat gac tcc atg agg gtc cta	1012
Gly Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu	
315 320 325	
tac tat atg gag aag gag cta gcc aac ttc gat cct tcc cgg cct ggc	1060
Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly	
330 335 340 345	
cct ccc aat ggc cga gtg gaa cgg gcc atg agt gaa gta acc tcc ctc	1108
Pro Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu	
350 355 360	
cat gaa gat gac tgg cga tct cgg cct tcc agg gct cct gcc ctc aca	1156
His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr	
365 370 375	
ccc atc agg gat gag gag tgg aat cgc cac tcc cct cgg agt ccc aga	1204



Pro	Ile	Arg	Asp	Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg	Ser	Pro	Arg		
		380					385					390					
aca	tgg	gag	cag	gaa	ccc	ctt	caa	gaa	cag	cca	agg	ggt	ggt	tgg	ggg		1252
Thr	Trp	Glu	Gln	Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly		
	395					400					405						
tct	ggg	cgg	cct	cgg	gcc	cgc	tct	gtg	gat	gct	cta	gat	gac	atc	aac		1300
Ser	Gly	Arg	Pro	Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn		
410					415					420					425		
cgg	cct	ggc	tcc	act	gaa	tca	gga	agg	tct	tct	ccc	cca	agt	agt	gga		1348
Arg	Pro	Gly	Ser	Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly		
				430					435						440		
cgg	aga	ggg	cgg	gcc	tat	gca	cct	ccg	aga	agt	cgc	agc	cgg	gat	gac		1396
Arg	Arg	Gly	Arg	Ala	Tyr	Ala	Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	Asp		
				445					450								
ctc	tat	gac	ccc	gac	gat	cct	aga	gac	ttg	cca	cat	tcc	cga	gat	ccc		1444
Leu	Tyr	Asp	Pro	Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser	Arg	Asp	Pro		
		460						465				470					
cac	tat	tat	gat	gat	ttg	agg	tct	agg	gat	cca	cgt	gct	gac	ccc	aga		1492
His	Tyr	Tyr	Asp	Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala	Asp	Pro	Arg		
	475					480					485						
tcc	cgt	cag	cga	tcc	cac	gat	cct	cgg	gat	gct	ggc	ttc	agg	tca	cgg		1540
Ser	Arg	Gln	Arg	Ser	His	Asp	Pro	Arg	Asp	Ala	Gly	Phe	Arg	Ser	Arg		
490					495					500					505		
gac	cct	cag	tat	gat	ggg	cga	ctc	tta	gaa	gag	gct	tta	aag	aaa	aaa		1588
Asp	Pro	Gln	Tyr	Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu	Lys	Lys	Lys		
				510					515						520		
ggg	gct	ggg	gag	aga	aga	cgc	gtt	tac	agg	gag	gaa	gaa	gaa	gaa	gaa		1636
Gly	Ala	Gly	Glu	Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu	Glu	Glu	Glu		
			525					530							535		
gag	gag	ggc	cac	tat	ccc	cca	gca	cct	ccg	cct	tac	tct	gag	act	gac		1684
Glu	Glu	Gly	His	Tyr	Pro	Pro	Ala	Pro	Pro	Pro	Tyr	Ser	Glu	Thr	Asp		
		540						545					550				
tcg	cag	gcc	tcg	agg	gag	cgg	agg	atg	aaa	aag	aat	ttg	gcc	ctg	agt		1732
Ser	Gln	Ala	Ser	Arg	Glu	Arg	Arg	Met	Lys	Lys	Asn	Leu	Ala	Leu	Ser		
	555					560					565						
cgg	gaa	agt	tta	gtc	gtc	tga	tcccacgttt	tgttatgtag	cttttatact								1783
Arg	Glu	Ser	Leu	Val	Val	*											
570					575												
tttttaattg	gaatattgat	gaaactcttc	accaagccta	ataaaa													1829

<210> 15  
<211> 1682

<212> DNA

<213> Mus musculus

<400> 15

gcaccgtcgc tgctagacgg ccgcg atg gcg ccg gcg gcc agc gcg tgt gct	52
Met Ala Pro Ala Ala Ser Ala Cys Ala	
1 5	
ggg gcg cct ggc tcc cac ccg gcc acc acg atc ttc gtg tgt ctt ttt	100
Gly Ala Pro Gly Ser His Pro Ala Thr Thr Ile Phe Val Cys Leu Phe	
10 15 20 25	
ctc atc att tac tgc cca gac cgt gcc agt gcc atc cag gtg acc gtg	148
Leu Ile Ile Tyr Cys Pro Asp Arg Ala Ser Ala Ile Gln Val Thr Val	
30 35 40	
cct gac ccc tac cac gta gtg atc ctg ttc cag cca gtg aca cta cac	196
Pro Asp Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu His	
45 50 55	
tgc acc tac cag atg agc aat acc ctc aca gcc cct atc gtg atc tgg	244
Cys Thr Tyr Gln Met Ser Asn Thr Leu Thr Ala Pro Ile Val Ile Trp	
60 65 70	
aag tat aag tcg ttc tgt cgg gac cgt gtt gcc gac gcc ttc tcc cct	292
Lys Tyr Lys Ser Phe Cys Arg Asp Arg Val Ala Asp Ala Phe Ser Pro	
75 80 85	
gcc agc gtg gac aac cag ctc aac gcc cag ctg gcg gct ggc aac ccc	340
Ala Ser Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro	
90 95 100 105	
ggc tac aac ccc tat gtg gag tgc cag gac agc gta cgc act gtc agg	388
Gly Tyr Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg	
110 115 120	
gtg gtg gcc acc aaa cag ggc aat gct gtg acc ctg gga gac tac tac	436
Val Val Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr	
125 130 135	
cag ggc agg aga atc acc atc aca gga aat gct ggc ctg acc ttc gag	484
Gln Gly Arg Arg Ile Thr Ile Thr Gly Asn Ala Gly Leu Thr Phe Glu	
140 145 150	
cag acg gcc tgg gga gac agt gga gtg tat tac tgc tcc gtg gtc tca	532
Gln Thr Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser	
155 160 165	
gcc caa gat ctg gat ggg aac aac gag gcg tac gca gag ctc att gtc	580
Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val	
170 175 180 185	
ctt gtt tat gct gct ggc aaa gca gcc acc tca ggt gtg cca agc atc	628
Leu Val Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile	
190 195 200	

tat gcc ccc agc atc tat acc cac ctc tct cct gcc aag act ccg cca Tyr Ala Pro Ser Ile Tyr Thr His Leu Ser Pro Ala Lys Thr Pro Pro 205 210 215	676
cct ccg cct gcc atg att ccc atg cgt cct ccc tat ggg tac cct gga Pro Pro Pro Ala Met Ile Pro Met Arg Pro Pro Tyr Gly Tyr Pro Gly 220 225 230	724
gac ttt gac agg acc agc tca gtt ggt ggc cac agc tcc cag gtg ccc Asp Phe Asp Arg Thr Ser Ser Val Gly Gly His Ser Ser Gln Val Pro 235 240 245	772
ctg ctg cgt gaa gtg gat ggg agc gta tct tca gaa gta cga agt ggc Leu Leu Arg Glu Val Asp Gly Ser Val Ser Ser Glu Val Arg Ser Gly 250 255 260 265	820
tac agg atc cag gct aac cag caa gat gac tcc atg agg gtc cta tac Tyr Arg Ile Gln Ala Asn Gln Gln Asp Asp Ser Met Arg Val Leu Tyr 270 275 280	868
tat atg gag aag gag cta gcc aac ttc gat cct tcc cgg cct ggc cct Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro 285 290 295	916
ccc aat ggc cga gtg gaa cgg gcc atg agt gaa gta acc tcc ctc cat Pro Asn Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser Leu His 300 305 310	964
gaa gat gac tgg cga tct cgg cct tcc agg gct cct gcc ctc aca ccc Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro 315 320 325	1012
atc agg gat gag gag tgg aat cgc cac tcc cct cgg agt ccc aga aca Ile Arg Asp Glu Glu Trp Asn Arg His Ser Pro Arg Ser Pro Arg Thr 330 335 340 345	1060
tgg gag cag gaa ccc ctt caa gaa cag cca agg ggt ggt tgg ggg tct Trp Glu Gln Glu Pro Leu Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser 350 355 360	1108
ggg cgg cct cgg gcc cgc tct gtg gat gct cta gat gac atc aac cgg Gly Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Ile Asn Arg 365 370 375	1156
cct ggc tcc act gaa tca gga agg tct tct ccc cca agt agt gga cgg Pro Gly Ser Thr Glu Ser Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg 380 385 390	1204
aga ggg cgg gcc tat gca cct ccg aga agt cgc agc cgg gat gac ctc Arg Gly Arg Ala Tyr Ala Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu 395 400 405	1252
tat gac ccc gac gat cct aga gac ttg cca cat tcc cga gat ccc cac Tyr Asp Pro Asp Asp Pro Arg Asp Leu Pro His Ser Arg Asp Pro His 410 415 420 425	1300
tat tat gat gat ttg agg tct agg gat cca cgt gct gac ccc aga tcc	1348

Tyr Tyr Asp Asp Leu Arg Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser	
430 435 440	
cgt cag cga tcc cac gat cct cgg gat gct ggc ttc agg tca cgg gac	1396
Arg Gln Arg Ser His Asp Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp	
445 450 455	
cct cag tat gat ggg cga ctc tta gaa gag gct tta aag aaa aaa ggg	1444
Pro Gln Tyr Asp Gly Arg Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly	
460 465 470	
gct ggg gag aga aga cgc gtt tac agg gag gaa gaa gaa gaa gag	1492
Ala Gly Glu Arg Arg Arg Val Tyr Arg Glu Glu Glu Glu Glu Glu	
475 480 485	
gag ggc cac tat ccc cca gca cct ccg cct tac tct gag act gac tcg	1540
Glu Gly His Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser	
490 495 500 505	
cag gcc tcg agg gag cgg agg atg aaa aag aat ttg gcc ctg agt cgg	1588
Gln Ala Ser Arg Glu Arg Arg Met Lys Lys Asn Leu Ala Leu Ser Arg	
510 515 520	
gaa agt tta gtc gtc tga tcccacgttt tgttatgtag cttttatact	1636
Glu Ser Leu Val Val *	
525	
tttttaattg gaatattgat gaaactcttc accaagccta ataaaa	1682

<210> 16  
 <211> 594  
 <212> PRT  
 <213> Mus musculus

<400> 16  
 Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro  
 1 5 10 15  
 Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp  
 20 25 30  
 Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val  
 35 40 45  
 Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn  
 50 55 60  
 Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg  
 65 70 75 80  
 Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu  
 85 90 95  
 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu

100					105					110					
Cys	Gln	Asp	Ser	Val	Arg	Thr	Val	Arg	Val	Val	Ala	Thr	Lys	Gln	Gly
		115					120					125			
Asn	Ala	Val	Thr	Leu	Gly	Asp	Tyr	Tyr	Gln	Gly	Arg	Arg	Ile	Thr	Ile
	130					135					140				
Thr	Gly	Asn	Ala	Gly	Leu	Thr	Phe	Glu	Gln	Thr	Ala	Trp	Gly	Asp	Ser
145					150					155					160
Gly	Val	Tyr	Tyr	Cys	Ser	Val	Val	Ser	Ala	Gln	Asp	Leu	Asp	Gly	Asn
				165					170					175	
Asn	Glu	Ala	Tyr	Ala	Glu	Leu	Ile	Val	Leu	Gly	Arg	Thr	Ser	Glu	Ala
			180					185					190		
Pro	Glu	Leu	Leu	Pro	Gly	Phe	Arg	Ala	Gly	Pro	Leu	Glu	Asp	Trp	Leu
		195					200					205			
Phe	Val	Val	Val	Val	Cys	Leu	Ala	Ser	Leu	Leu	Phe	Phe	Leu	Leu	Leu
	210					215					220				
Gly	Ile	Cys	Trp	Cys	Gln	Cys	Cys	Pro	His	Thr	Cys	Cys	Cys	Tyr	Val
225					230					235					240
Arg	Cys	Pro	Cys	Cys	Pro	Asp	Lys	Cys	Cys	Cys	Pro	Glu	Ala	Leu	Tyr
				245				250						255	
Ala	Ala	Gly	Lys	Ala	Ala	Thr	Ser	Gly	Val	Pro	Ser	Ile	Tyr	Ala	Pro
			260					265					270		
Ser	Ile	Tyr	Thr	His	Leu	Ser	Pro	Ala	Lys	Thr	Pro	Pro	Pro	Pro	Pro
		275					280					285			
Ala	Met	Ile	Pro	Met	Arg	Pro	Pro	Tyr	Gly	Tyr	Pro	Gly	Asp	Phe	Asp
	290					295					300				
Arg	Thr	Ser	Ser	Val	Gly	Gly	His	Ser	Ser	Gln	Val	Pro	Leu	Leu	Arg
305					310					315					320
Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Glu	Val	Arg	Ser	Gly	Tyr	Arg	Ile
				325				330						335	
Gln	Ala	Asn	Gln	Gln	Asp	Asp	Ser	Met	Arg	Val	Leu	Tyr	Tyr	Met	Glu
			340					345					350		
Lys	Glu	Leu	Ala	Asn	Phe	Asp	Pro	Ser	Arg	Pro	Gly	Pro	Pro	Asn	Gly
		355					360					365			
Arg	Val	Glu	Arg	Ala	Met	Ser	Glu	Val	Thr	Ser	Leu	His	Glu	Asp	Asp
		370				375					380				
Trp	Arg	Ser	Arg	Pro	Ser	Arg	Ala	Pro	Ala	Leu	Thr	Pro	Ile	Arg	Asp
385					390					395					400
Glu	Glu	Trp	Asn	Arg	His	Ser	Pro	Arg	Ser	Pro	Arg	Thr	Trp	Glu	Gln

405								410				415			
Glu	Pro	Leu	Gln	Glu	Gln	Pro	Arg	Gly	Gly	Trp	Gly	Ser	Gly	Arg	Pro
			420						425				430		
Arg	Ala	Arg	Ser	Val	Asp	Ala	Leu	Asp	Asp	Ile	Asn	Arg	Pro	Gly	Ser
		435					440					445			
Thr	Glu	Ser	Gly	Arg	Ser	Ser	Pro	Pro	Ser	Ser	Gly	Arg	Arg	Gly	Arg
	450					455					460				
Ala	Tyr	Ala	Pro	Pro	Arg	Ser	Arg	Ser	Arg	Asp	Asp	Leu	Tyr	Asp	Pro
465					470					475					480
Asp	Asp	Pro	Arg	Asp	Leu	Pro	His	Ser	Arg	Asp	Pro	His	Tyr	Tyr	Asp
				485					490					495	
Asp	Leu	Arg	Ser	Arg	Asp	Pro	Arg	Ala	Asp	Pro	Arg	Ser	Arg	Gln	Arg
			500						505				510		
Ser	His	Asp	Pro	Arg	Asp	Ala	Gly	Phe	Arg	Ser	Arg	Asp	Pro	Gln	Tyr
		515					520					525			
Asp	Gly	Arg	Leu	Leu	Glu	Glu	Ala	Leu	Lys	Lys	Lys	Gly	Ala	Gly	Glu
	530					535					540				
Arg	Arg	Arg	Val	Tyr	Arg	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	His
545					550					555					560
Tyr	Pro	Pro	Ala	Pro	Pro	Pro	Tyr	Ser	Glu	Thr	Asp	Ser	Gln	Ala	Ser
				565					570					575	
Arg	Glu	Arg	Arg	Met	Lys	Lys	Asn	Leu	Ala	Leu	Ser	Arg	Glu	Ser	Leu
			580						585				590		
Val	Val														

<210> 17  
 <211> 575  
 <212> PRT  
 <213> Mus musculus

<400> 17  
 Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro  
 1 5 10 15  
 Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp  
 20 25 30  
 Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val  
 35 40 45  
 Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn  
 50 55 60

Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg  
 65 70 75 80  
 Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu  
 85 90 95  
 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu  
 100 105 110  
 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly  
 115 120 125  
 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile  
 130 135 140  
 Thr Gly Asn Ala Gly Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser  
 145 150 155 160  
 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn  
 165 170 175  
 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp Trp Leu Phe Val Val  
 180 185 190  
 Val Val Cys Leu Ala Ser Leu Leu Phe Phe Leu Leu Leu Gly Ile Cys  
 195 200 205  
 Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys Tyr Val Arg Cys Pro  
 210 215 220  
 Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala Leu Tyr Ala Ala Gly  
 225 230 235 240  
 Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr  
 245 250 255  
 Thr His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro Ala Met Ile  
 260 265 270  
 Pro Met Arg Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg Thr Ser  
 275 280 285  
 Ser Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg Glu Val Asp  
 290 295 300  
 Gly Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn  
 305 310 315 320  
 Gln Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu  
 325 330 335  
 Ala Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu  
 340 345 350  
 Arg Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser  
 355 360 365

Arg Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp  
370 375 380

Asn Arg His Ser Pro Arg Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu  
385 390 395 400

Gln Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg  
405 410 415

Ser Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser  
420 425 430

Gly Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala  
435 440 445

Pro Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro  
450 455 460

Arg Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Leu Arg  
465 470 475 480

Ser Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser His Asp  
485 490 495

Pro Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg  
500 505 510

Leu Leu Glu Glu Ala Leu Lys Lys Lys Gly Ala Gly Glu Arg Arg Arg  
515 520 525

Val Tyr Arg Glu Glu Glu Glu Glu Glu Glu Glu Gly His Tyr Pro Pro  
530 535 540

Ala Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg  
545 550 555 560

Arg Met Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val  
565 570 575

<210> 18

<211> 526

<212> PRT

<213> Mus musculus

<400> 18

Met Ala Pro Ala Ala Ser Ala Cys Ala Gly Ala Pro Gly Ser His Pro  
1 5 10 15

Ala Thr Thr Ile Phe Val Cys Leu Phe Leu Ile Ile Tyr Cys Pro Asp  
20 25 30

Arg Ala Ser Ala Ile Gln Val Thr Val Pro Asp Pro Tyr His Val Val  
35 40 45



Ile Leu Phe Gln Pro Val Thr Leu His Cys Thr Tyr Gln Met Ser Asn  
 50 55 60  
 Thr Leu Thr Ala Pro Ile Val Ile Trp Lys Tyr Lys Ser Phe Cys Arg  
 65 70 75 80  
 Asp Arg Val Ala Asp Ala Phe Ser Pro Ala Ser Val Asp Asn Gln Leu  
 85 90 95  
 Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr Asn Pro Tyr Val Glu  
 100 105 110  
 Cys Gln Asp Ser Val Arg Thr Val Arg Val Val Ala Thr Lys Gln Gly  
 115 120 125  
 Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly Arg Arg Ile Thr Ile  
 130 135 140  
 Thr Gly Asn Ala Gly Leu Thr Phe Glu Gln Thr Ala Trp Gly Asp Ser  
 145 150 155 160  
 Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln Asp Leu Asp Gly Asn  
 165 170 175  
 Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Val Tyr Ala Ala Gly Lys  
 180 185 190  
 Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr Ala Pro Ser Ile Tyr Thr  
 195 200 205  
 His Leu Ser Pro Ala Lys Thr Pro Pro Pro Pro Pro Ala Met Ile Pro  
 210 215 220  
 Met Arg Pro Pro Tyr Gly Tyr Pro Gly Asp Phe Asp Arg Thr Ser Ser  
 225 230 235 240  
 Val Gly Gly His Ser Ser Gln Val Pro Leu Leu Arg Glu Val Asp Gly  
 245 250 255  
 Ser Val Ser Ser Glu Val Arg Ser Gly Tyr Arg Ile Gln Ala Asn Gln  
 260 265 270  
 Gln Asp Asp Ser Met Arg Val Leu Tyr Tyr Met Glu Lys Glu Leu Ala  
 275 280 285  
 Asn Phe Asp Pro Ser Arg Pro Gly Pro Pro Asn Gly Arg Val Glu Arg  
 290 295 300  
 Ala Met Ser Glu Val Thr Ser Leu His Glu Asp Asp Trp Arg Ser Arg  
 305 310 315 320  
 Pro Ser Arg Ala Pro Ala Leu Thr Pro Ile Arg Asp Glu Glu Trp Asn  
 325 330 335  
 Arg His Ser Pro Arg Ser Pro Arg Thr Trp Glu Gln Glu Pro Leu Gln  
 340 345 350

Glu Gln Pro Arg Gly Gly Trp Gly Ser Gly Arg Pro Arg Ala Arg Ser  
 355 360 365  
 Val Asp Ala Leu Asp Asp Ile Asn Arg Pro Gly Ser Thr Glu Ser Gly  
 370 375 380  
 Arg Ser Ser Pro Pro Ser Ser Gly Arg Arg Gly Arg Ala Tyr Ala Pro  
 385 390 395 400  
 Pro Arg Ser Arg Ser Arg Asp Asp Leu Tyr Asp Pro Asp Asp Pro Arg  
 405 410 415  
 Asp Leu Pro His Ser Arg Asp Pro His Tyr Tyr Asp Asp Leu Arg Ser  
 420 425 430  
 Arg Asp Pro Arg Ala Asp Pro Arg Ser Arg Gln Arg Ser His Asp Pro  
 435 440 445  
 Arg Asp Ala Gly Phe Arg Ser Arg Asp Pro Gln Tyr Asp Gly Arg Leu  
 450 455 460  
 Leu Glu Glu Ala Leu Lys Lys Lys Gly Ala Gly Glu Arg Arg Arg Val  
 465 470 475 480  
 Tyr Arg Glu Glu Glu Glu Glu Glu Glu Gly His Tyr Pro Pro Ala  
 485 490 495  
 Pro Pro Pro Tyr Ser Glu Thr Asp Ser Gln Ala Ser Arg Glu Arg Arg  
 500 505 510  
 Met Lys Lys Asn Leu Ala Leu Ser Arg Glu Ser Leu Val Val  
 515 520 525

<210> 19  
 <211> 22976  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> exon  
 <222> 1898..2253

<221> exon  
 <222> 3437..3781

<221> exon  
 <222> 12065..12184

<221> exon  
 <222> 15045..15101

<221> exon  
 <222> 15666..15812

<221> exon  
 <222> 19479..19652  
  
 <221> exon  
 <222> 19799..19858  
  
 <221> exon  
 <222> 19956..20087  
  
 <221> exon  
 <222> 20229..20854  
  
 <221> exon  
 <222> 20944..21094  
  
 <221> Misc\_Feature  
 <222> 19956..19958  
 <223> Potential variant splicing site AAG

<400> 19  
 aacagtttgg cagttcctca aaagggttaa aatagaacta ccaagtcacc cagcaattcc 60  
 attcttaggc atatattcaa aagaaatgaa agcagatatt tgtacaccag tggtcacagc 120  
 tgcactatTTT acaatagtca aaaggtagaa acaacctagg tccatccaca aatgaatgga 180  
 taaataaaac gtagcatata catacaatgg tacactagtc cgctgtaaaa agaaattttg 240  
 atcttactgc atgctacatg gcttcgacat actacaacat ggatggacct tgaaaacatt 300  
 attctttgtg aaataaacta gacacaggac aaatgttaga cgattccact tatatgaggc 360  
 acctagaatg ggcaatttgg taagcaaagt agaatagaaa ttactagggg cacaggtagc 420  
 agggaatggg gagttactgt ttaatggtca cagagtttat gttggggatg atgaaacagt 480  
 ttcggggata aagagtgggtg attggtacac gacattgtga atatacttaa tgccactgaa 540  
 ttttacactt gaagtgggta aagcgataaa tattatagtt tgcataTTTT atcataaaaa 600  
 tatttttttta aacgatgaag ggacgtgaac ggggttgaaat tttataaaaa gtggccaggg 660  
 aaggtgtcac tgcaatgggtg tcctacagga ggaggaagat catgtggaca tctgcgggaa 720  
 ggggtgttctg gcagagggag tagcacgggc gatggctctg aggactgtga gaagtatagt 780  
 tggaacagc gaggaggcca ggggtgtccga agctgagtaa gccagagaga gtgggaggag 840  
 gtgagataag agggggaagg tcagtttctg ctgagagtga ggaggagcca caggagggct 900  
 gtgagcaggt ggacgtgatc tggcttgagt tttaacaggg ccagtagaac aaagcacgcc 960  
 tgggtaccga aaccagccac tggccagttg gcaacctggg ggagtctaac gcgaggaagc 1020  
 gcccagggtt ccccaggat gcgctttccc tcgccgccac ctggagacag cagagtcacg 1080

cccagcgctg cgcaggctga tcgccgcgcc gcgccccgc cctcggtcgc aggtggctcg	1140
ttccgggaat tcctaagcgg aaaccggtcc caagccccgc gccttcgctc ggccccttta	1200
agagccagaa tttccggagg gctgacccgg gggctagggg tgcccagggg ccgaaccaca	1260
agttgggaac ggggtggggg ggtggcgaaa acttccgaag tggaattcca acttttcctg	1320
gccctgattc cccttgggca tccctgaggg ggcagagctt cccttcggg gactttagag	1380
ggttcctcag gtcattctaac tgggagacac aggaggcccg aagcgcccc cctccaccg	1440
gtccggagga accccagtgg aagtggagaa gtcaggcgcc accaacaagc ctctcccagc	1500
caggactttg cttagactcg ctctcccgg cagggcgcac ctaggcgggt ccatcgccag	1560
ccggggagag gggtttgggc agggagggaa cagggtgcgc gcgggaccg ccctatctca	1620
acaggtgaat cgctccaagt gggctctcgt tgcattggat tcgggtgcgt tggtttgcc	1680
ggagcagatg ggggcccggaa gggacctgtg gtccgcaggc gccctcccag cgggccagtc	1740
acttggttcg ggccctgggg gacggagcgc acctgggtca gccacttcc ggggagggag	1800
gcagaggaac ccctccccgc cgctcaccgc taagcccagc cctcggctcc cacccttggtg	1860
tacctgggcc gaaccattca ccggagcgcg cagcgggtgg agtgtggctc ggaggaccgc	1920
ggcgggtcaa gcacctttct ccccatatc tgaaagcatg ccctttgtcc acgtcgttta	1980
cgctcattaa aacttccaga atgcaacagg acggacttgg agtagggaca aggaacggaa	2040
gtgggaaggg gaggagcgtg caccctcct ggccttggtg cgcgccgcgc ccctaaggt	2100
actttggaag ggacgcgcgg gccagacgcg ccagacggc cgcgatggcg ctgttggccg	2160
gcgggctctc cagagggctg ggctcccacc cggccgcgc aggccgggac gcggtcgtct	2220
tcgtgtggct tctgcttagc acctggtgca caggtacggg gcacggggcc tctgacgctg	2280
cggaaacgcc gagggaaactg tagaggggga tggatggagt tggaggcggc gggaagcggg	2340
aagcgggggt ctcaaggct gggaccttcc gatcccctgg gtcttgggcg atctgttgcg	2400
cgcgggagtg agaggaattc cccatttggt ccggggagcg ctccccgcgc ccttatctgg	2460
aagatagcag gaagtgaac tccctggacg gtgagacccg gagcggcagg gagaatggaa	2520
ctctttgtgg ggaggagtg gaagaccgcc cgatctctgg gaaaagaaaa gccgggatgg	2580
gacttgggcg caccggggg tttctaagtt ttggagtaac ggggagaggg cacgggaggg	2640
ctggatcaga cgcttcctag agggacagag acgaaggaac aatgcctagg cctcgggtgg	2700
gtgtgggact ggggactccc catccccgc accccacca cctccgcgg gctccggatt	2760
atacgtgcgt aagagtctgg tgggatggat ttacggactt gaaaccgact tctgctggca	2820

ggctttcacc tggatgggat atttgggtgg tgatgaggtc tttcccgaga cacttttggg	2880
tcagtcattt gaaatgactt tagagtaggg tgaggtgggt ggaggctgat ggagatattg	2940
tgggggcttt agtcctcca tggcaaagca gttcaggcaa acaactccat ggttttccct	3000
ccaaattcaa aaggccccgg gtaacctgga atccttcgta gtcggttttg aagtggggcc	3060
ttgggcgctg ggggcatcaa catggccatc tgggcttgcc tgcccaggcc acacagaggc	3120
cccttgttgt gggatgaatgg caaagggaag aggggactgg tgtggttcag aggccacagg	3180
ctgggaagag ggatggcggg cgagtccaag gaaactggcc gtgtcaccgt gcacctgcca	3240
cttcagcccc acgggtctat aaaatgggca tgattatcgt ggctacctca ctggctcctg	3300
caattaagga acaatgtgtg ccaggcactc tgtaaaccac atacttgca gtgtcaagct	3360
ggtgacaggt ggcgttcctg ttgaagcacc tccctgagct cacagcaacc cttgctgtct	3420
ctcctcttgc cctcagctcc tgccagggcc atccagggtga ccgtgtccaa cccctaccac	3480
gtggtgatcc tcttcagcc tgtgacctg ccctgtacct accagatgac ctcgaccccc	3540
acgcaacca tcgtcatctg gaagtacaag tctttctgcc gggaccgcat cgccgatgcc	3600
ttctccccgg ccagcgtcga caaccagctc aatgccagc tggcagccgg gaaccaggc	3660
tacaaccct acgttgagtg ccaggacagc gtgcgcaccg tcagggtcgt ggccaccaag	3720
cagggaacg ctgtgacct gggagattac taccagggcc ggaggattac catcaccgga	3780
agtatggttg gcagggcagg gggatgaggc tgggcttgcc cgggtgggtg gactggcgtc	3840
cttgtgcggg acctggagtc cccatctgaa agctcttgag tgccagtgtc tgaaaggacc	3900
attgaaggga gcaattcttt tttttttttt ttttgaagat ggagtcttgc tctggactcc	3960
aggctggagt gcagtgggtg gatctcagct cactgcaacc tccacctccc aggttcaagc	4020
aattctcttg cctcagcctc ccgagtagct gggactccag gtgcgtgcca ccacgcccag	4080
ttaatttttg tatttttagt agagatgggg ttccaccatg ttggccaggc tggctctaaa	4140
ctcctgacct caaatgatct gccgccttg gcctcgcaaa gtgctgagag acaccatacc	4200
cagcctaaag ggagcgattc tattctacta ttcttccttc tgctaatact tccattcttt	4260
aatttaataa cgaagatttt ttgagtacct gtcatatacc aggtgctgtt ctgggccctg	4320
ggaatacagc tgtaacaaa atcatcaaac cacttccctc gtggagccca cattgcagtg	4380
agagagacaa acacgacaca cactctcaag tccttgaaga taaagaaaac tgggtaacgg	4440
agagaagagg ccagggtttg ttctataatc attaataaca cgagcagtaa gaagtaaat	4500

ttatctaagt aacaacttat aaaggggtcta ctgtgtgcta agctctcatc caggttccca	4560
aggattaact cagaccacac agtaattgaa tagattctat cattgtcatc ttacagaggc	4620
ccagagagag aaagtgactt gcctagtgtc atagctggta acggggctgg gattctaact	4680
cagccacttt gggctctagt gccaagctcc taatcccttt gcttgcctag ggtgggccgc	4740
agaggactca cagaggagat ggcaggagt gaaactgcaggg gcaagagagc ttaatggaga	4800
aagcctgtga catgccagga actgcacaca tattctccca ttgagtcctc tcctctaccc	4860
tcctgacagc tgaggcacag agaggttacc ttgttcaa at ggggtgcatag gaagtcaaag	4920
tctggagctg gggtttgaac ccaggcagcc ctgagaacct tgttcttttt ttttgagacg	4980
gagtctcgct ctgtcgccca ggctggagt gacgtggcggg atctcggtc actgcaactc	5040
cgctccccgg gttcacgcca ttctcctgcc tcagcctccc aagtagctgg gactacaggc	5100
gcccgcact acgcccggct aatTTTTTgt atTTTTtagta gagacggggg ttcaccgttt	5160
tagccgggat ggtctcgatc tcctgacctc gtgatccgcc cgctcggcc tcccaaagt	5220
ctgggattac aggcgtgagc caccgcgcc ggccccttgt tcttaactgt aatgctgcct	5280
cctgatagga tgtgcctgtt gggactaagt aaggggcagt cattcattca ttcatttggt	5340
atttatcaag catcgactat gtgtcggttg tgctggggat agaggtgatt gggatggctg	5400
aagtttctgt cgtcaaggag atgacattct ggtggagtga gactggcagt aaataagcag	5460
ataaagaaag agtatgagaa tttcaaagtc tgggcacggg ggctcacgtc tgtaattctca	5520
gcactttggg aggccaagggt ggggtggatca cctgaggtca ggagttccag accagcctgg	5580
ccaacatggg gaaaccccgt ctctactaaa aatacaaaga ttagccaggc atgggtggcac	5640
atgcctgtaa tcccagctac tcaggaggct gaggcattgag aatcgcttga acccaggagg	5700
cagaggttgc agtgagctga gatcgacca ctgtactgca gtctgggcga cagagtgaga	5760
ctctgtctca aaaaaaaaaa aaaaaaaaaa gactccgtca aggtataaga atgtcagaga	5820
gtactaagtg ttgcaaagaa aataacacca ggctgggtgc attggctcat gcctgtaaat	5880
ttcagcactt tgggaggcca aggcaggagg atcacttgag cctaggagtt tgagaccagc	5940
ctggacaaca aatgagacc ccatgtctac aaaaatttta aaaatttaaa aattagctgg	6000
gcatgggtggc atgtgcctgt ggtcccggct gctcaggagg ctgaggtggg aggattgctt	6060
gggcttgaga ggtcaaggct tcagtgagtc atgatcgtgc cactgcattc cagcctgggt	6120
gacagagtga gaccctgtct tgaaatgaaa agaaaatagg ctgggcgcag tggctcacac	6180
ctgtaatccc agcactttgg gaggccgagg tgggtggatc acctgaggtc aggagatcga	6240

gaccagcctg gccaacatgg tgaaatccca tctctactaa aaatacaaaa tttagccggg	6300
cgtggtggtg ggcgcctgta atcccagcta ctcgaggaggc tgaggcagga gaatcgcttg	6360
aacctgggag gcgaagggtg cgggtgcgcca agattgcgcc actgcactct agcctgggaa	6420
acagtgagac tccgtcttaa aaaaaaaga aaaaagaaaa tagcactggg tgatgtgcta	6480
catggaatga cttgggctgt gaatatgatt tgaggagggc ctgggcctgg gccttacaga	6540
acctagaagg cagagaggaa ggggaggggc agggtgccag ggatgaaggc tcacgtacct	6600
catgtcttag tgtgtgttca ctgtcttaaa caagaattta aagttgggca tggggcagag	6660
cggggaaggg agcatccctt tgcagacccc aagaagccag gaactggagc acattctgct	6720
agaggatcga tgggaagcag ggttccaggg gctgagccta tgtcagtcct gtttcagagg	6780
aggcaccagg cttgcttgcc ctgaatttct gtgggcagct cagccatgag catcctactg	6840
ttattgaggt cacagggtg cttaggcccc ctctctctta acccagggat tgtgcctgcc	6900
tggaccaggc gtgactgcta agcttctgcc aggacaagcc aaatactgag ggtgcttcct	6960
ctgctggacg caaaagtcca ggatgacccc ccaggctctg tctcggggaa ggggccctgc	7020
atgctccagg ggcctcacag gcctgggtct ttcaaaccac cccacctgg gcctgtgttt	7080
gatcaaggcc ctgagtgtaa acatccattg tgtgtgtcct ttcaggaaat cccatagcca	7140
taggagcttc ctctgtttca gctttgagga tggggaaaag tggactcccc gtggtgttcc	7200
tagggtcacc cactgtgctg gggtttttct gttgttggtg ttttttttct gttgcccagg	7260
ctggagtgca gtggtgcaat ctgagctcac tgcaacctct gcctcgcaag ttcaagtgat	7320
tctccgcctc agcctcctga gtagctggga ttacagggtgc acaccaccac acctggctaa	7380
tttttgtatc tttttggtag agatgggatt tcgccatgtt ggccaggctg gtctcaaact	7440
cctgacctca ggtgatctgc ctgccttggc ctcccaaagt tctgggatta cagatgtgag	7500
ccaccatgcc cggcctatcc tggtttcaaa agtgaaaata gtccctggata aggtagaagg	7560
ctgtccactc caggcatccc tccgggtccgg tggctcattc cctgctttgt ccttccatgc	7620
tttgggtgat ggaccagcac ctggacagga ggccctgttc cacctcctcg ggctccttgg	7680
ggtccaagtg cccccacctc cagctgcact gcagcagaga gcccatggga cctctgaaat	7740
catgaaggtc acctttgcgg tgtataaaga aggaaccaga ggttgagat gtggaggagg	7800
cctggctgct gttcccactg gagacctggc atcttctccc cgacctaaaa caatgaaagc	7860
agtgctcagc ccggatgaga tcacggccag cccaagacca ggaacagggt acgccctgca	7920



ggaagaaggt gtgcccagac cttaggatgg atcaaaagaa gccggaaaac tatatTTTTT	7980
gtgagTTTTg aaaatgtcag acaggtcaaa caaaacacag tgaggtccag cctcggccta	8040
caagatgcc a gatttcaacc cctggcctat atgatctgtt tgccatggca ggcgggtcct	8100
gtccacctct tttgtttata gcagggacca gctcttgagc tccagtgttg aagaggcacg	8160
gtcagggctc gatctgaaga cactgggtggc tcatgcctgt aatcccagca cttcaggagg	8220
ccgaggcagg aggattgctt gaggacagga gctgggagac cagcctgggc aacacagtga	8280
gaccagaga ctacaaaaaa ataaatttag cggggcatga tggcacaccc tgctactctg	8340
gagatgggaa gattgcttga gcctaggagt tcgaagctgc agtgacccat gatcgacca	8400
ctgcactcca gcctgggcca ccaagctagg ccctctcaaa aaagatacag gtggaaaaat	8460
gatggacgaa gagggcattg tggcaaacct ggggatttag gagaacctag tttggaattc	8520
tatgaggatt caatgaaaga atgtgtgtag aggggccag cacatagtaa gagctcaata	8580
aacggtgggg gctagggggc gtggctcatg cctgtaatcc cagcactttg ggaggctgag	8640
gcaggtggat cacttgagcc ctggagttca agatcaacct ggacaacaaa gcaagatccc	8700
atctcaaaat taaaaaaca caccaacaac aaaaaaacag tggcttagat gcctgatcat	8760
tagggtaagt cgtgtcctca accccttcac atctgctctg aaggtcacca tatccggaag	8820
ccttcctgg cctccttggt taaaatggca cagccccac tccacgcctg gcactctctg	8880
ctgtccctga ttcgttttct ccatacagct tatctttgtc tgatatgtga catagttaac	8940
attttatatt tgtctttctt tcctagttag aatctgaact ctagaagggc aagggaagg	9000
atttataact caaagggtcc gggcttaggc ctcttttata ttcttgattt tgaggttaat	9060
taagagctca ggcctagcga ggtggctcat gcctggaatc ccagcacttt gggaggccca	9120
ggcgggcaga tcacttgagg tcaggagttc cagacctgcc tggccaacac agtgaaaaac	9180
ctgtctctac taaaaataca aaaattagcc agttatgttg gcaggcgcct ataatcccag	9240
ctactcaaga ggctgaggca ggagaatcgc ttgaaccag gaggcagagg ctgcagtgag	9300
ccaagatcgt gccactgcac tccagcctgg gcaacagagc gagactccat ctcaaaaaaa	9360
aaaaaaaaat taagagctca aagagtttgt tttcataggc agcagaatga gaaaagtta	9420
caaatagtt taaatgacaa taaagtcatt atagattaac ataaataaaa taccttttat	9480
gaaaaaata atcattttct gaaatcagac aaaacattgt gaatgagaag gtggcatggt	9540
tttatTTTT tgcaagtctc cgaagcctgg ctggatagaa gagcctggct tctcagagct	9600
gcttcagtct gttgtgatat ctattgtatg tcacgtagcc tctggaaaac tccacagtta	9660



gtattgttgg gaaaataact ttgacctcag gatctcctga aaacgtcttg gggaacccca	9720
gggtctagag gctgcagttt gagaactggt gctgtggtat cccaggtgtc tcaaatactg	9780
cctagaacat aggtggtact cagtaattat tgttgaagga tgaatgaatg aatgaatgaa	9840
tgaatgaatg aaagaaagaa agaaatgtgt ctttgaatcc agccatgtgc ccagaatgat	9900
gagacagatg acaaaagcta agggacttta gcatgaggag aggggggttcg tttccttttt	9960
tttctttttt ttttgagatg gagtctcact ctactgcca ggctagagtg cagtgggtgca	10020
atctcagctc actgcaatct ctgcctcctg agttcaagca attctcctgc ctcagcctcc	10080
agggtagctg ggactacagg tgcgtgccac catgcctagc taatttttta catttttggt	10140
agagatgggg ttttaccatg ttggccgggc tgggtctggaa ctctgacct caagtgatcc	10200
acctgcctca gcctcccaaa gtgttaggat tacaggtgtg agccaccatg tccggccaag	10260
agggtgttca tttctgctcc ttgccaggta ttgtgtcagg cactggggac ccagcagtgg	10320
ctgagacaga cagggtctctg cctcacggag cccacatttt caccaggcaa aggatggtcg	10380
gcccctaagc tgggagataa gacttcagca gttgggtggg ggagccgtgg gagaagccca	10440
gcccacaggg ggacagtgca aatctagaac caaggcgatg gcaggggtga ggctggcacg	10500
gtagctagag accacgtcgt gccaagggcc ttggggacca tgggactatg ggaccttagg	10560
gaaggcgtct ggaatgctgt agccagacac tgttgcaagg aggatttttc tgtagacatg	10620
aggccttcct tatgaagaaa gcaagggttc tttcattcct gggggtgcca ggtgctgtgg	10680
actgcagcac gcgtggttgc tgccgtcaca gagctgtcat gcaggagggc agcgcgtcct	10740
tgggaagggtg gcaggcaggt caggctagga ggaaagaggc cgggaagctg agggcatttc	10800
ctgcccgaga tgcccaatgt agcctacttc tgtccccagt ggcttaaggc agagttgcct	10860
ggtaggtgcc ctggtcccac cctggtgaaa ggctgaagggt atttaattag tgcctgagaa	10920
gcagagagga aacaggatgt gccaaaacac tttgatggat ggtagagtta acaggctcct	10980
tgcctgcagc tgcttcagac aagagcgtcc ccaagccctg ggcctgacct ggaatgtggg	11040
gatggaaggg gagggggagg aaccaaggca ctgggagggt aagtctctct ctcccacata	11100
gacacacca ctcttatgg gtgcctgggc atctcctggt acctagaatc tggcctgttt	11160
atctccacac ccctccctgg ggtctacact aggcctgtg ggtggcagtt cacatcaggg	11220
gagttctgac tttggctctg agagggtggt cagagatggc tgtaagttga gaagcacaga	11280
ctgctgggtg tgggtggttca cgcctgtaat cccagcactt tgggaggctg aggtgggggt	11340

ggatcacctg aggtctggag ttcaaaacca acttgggtcaa catggcgaaa ctccatctct 11400  
 actaaaaatg caaaaattag ccaggtgtgg tggcaggtgc ctataatccc agctacatgg 11460  
 gaggtgagg caggagaatt gcttgaatct gggaggcgaa gattgtagtg agccgagatt 11520  
 agttcgcacc attgcatgcc agcctgggca acaagagtga aactccgatt caaacaaaaa 11580  
 aaaaaaaaaag ctgggcatgg tggagtgcct gtagtcctaa ctactcaggt gggaggattg 11640  
 cttgagtcca ggaggttgaa gttgcagtgg gctataatta caccactgca ctccagccag 11700  
 ggccacagag tgagaccctg tctctaaaga aagaaaaaaa aaaacaacct caggctccga 11760  
 gggcaccatt actgctctat actgaagagc tgtgcagctt ttccagaccc gaaatgtcat 11820  
 ccacaaaaca gaagtataa tggtcctgcc tcacagactt cttgcagtag tccaggtgtt 11880  
 tagaacgggg tgtaaaaggc cgtgtgccct tggtaggaat ctttgcatat gcatttgatc 11940  
 atctgcagcc tgcccagccc actgcttgcc ccctcctggg tgtgctggga aggggtcttt 12000  
 ggcctccag gggttaggtg cccagcctc caaggtgccc tcacgccttt tcatcccgac 12060  
 tcagatgctg acctgacctt tgaccagacg gcgtgggggg acagtgggtg gtattactgc 12120  
 tccgtggtct cagcccagga cctccagggg aacaatgagg cctacgcaga gctcatcgtc 12180  
 cttggtgagt gggcctggga agggggaggc atggcccttc cttttgtccg cttctgttct 12240  
 gtctgccctc ccctgtgtcc gccctctgcc ctccagctta ccctctgggc tctgtgcct 12300  
 gctctgctct ccccaggct ctgccagtca cttaggctcc cctgtgccct gcaccccagg 12360  
 cagggaccac tggcccacag tgctccaat cacccaagcc aaactaagag aagagtggag 12420  
 acaattggag actctgcctt ttcaaagtct catttttaaa aaaaatccag acttggggtc 12480  
 cgggtgcggt agttcatgcc tgtaatccca gcactttggg aggccgaggc gggtagatca 12540  
 cttgaggcca ggagttcgag actagcctgg ccaacgtggc aaaatcccgt ctctataaaa 12600  
 aatataaaag ccaggcgtgg tgggtgcacat gcctgtaatc ccagttactc agaaggctga 12660  
 ggcatgagga ttgcttgaac ctgggaggca gaggatgcag taagccaaga tcaagccact 12720  
 gcactccagc ctgggcgaca gagtgagact ctgtccaaaa aaaaaaaaaa tccagacgtg 12780  
 gtcagagtcc atgggcagtg aatgaggaca gttgatggtg tgcaaaatcg acccacctct 12840  
 tgctacatcc ccaaggcctc atctcaccog agtccctcgc caaagcacag cggttttgcc 12900  
 gtgtgccctg ctgggatggc gctgcatggc acacacactg tgtaagtttg agtgcagctg 12960  
 aaacgaagcc gattccagac acccaggggc agggcggggt gtccgtgtgg ctgggaggcc 13020  
 tccttgtgtt agggggatgt tgccatcggc caggtgccct gctgtaagcc aacacatgga 13080

gtcttgatg acatgtgctc tgcattgagt atgccgctgg gctgtacact gccatcttca 13140  
 catgtgtgaa tgagcacgtg actgggggggt acttggggctg caagacagag ttcattgtgtg 13200  
 ggggatggaa cacgtgcacc agtgacccag gaacctctgc ctgttcttcg gtaaaatgca 13260  
 ccatttgcat cagcagttcc caaaattagt ctccaggtct atttacactc taaaacatta 13320  
 tcgaggggtct ccaagagctt ttgtttgttt ctgtgggttt tatgtctatc tgttgcttaa 13380  
 catattagga attaaaatgg ggagattttc cttttttttt tttttttttg agatggagtc 13440  
 tcgttctgtc gccagggctg gattgcagtg gctcgatctc ggctcactgc aagcttcacc 13500  
 tcctgggttc acgccattct cctgcctcag cctcccaggt agctgggact acaggcacc 13560  
 gccaccacac ccggctaatt ttttttgat ttttagtaga gactgggttt caccatgtta 13620  
 gccaggatgg tctcgatctc ctgacctgt gatccacca cctgggcctc ccaaagtgt 13680  
 gggattacag gcatgagcca ctgcccgcc ttaaaatggg gagatttttc aagcccaaga 13740  
 tacacaagga agactgggca acatggcaag accctgactc tacaaaaaat tttaaaatta 13800  
 accaggcatg gtggcatgca cctgtgagcc cagcttcttg ggaggctgag gcaggagtat 13860  
 cgcttgcacc caggaggtca aggctgcagt gagccgtgac tatgtactg cactctagca 13920  
 tgagtgcag agacctggc tcaagaaaca caaacacaca cacacacaca cacacgcata 13980  
 tagtccatta ggcattcagg cgatgatggc atcagggagc ctgggaaact ctactggaca 14040  
 ttcattgggag aacaagtga aaaggcaaat aacattctag tgttattcta aaatttcttc 14100  
 ttttggcctt gtggacagga ccacgctttg agagctgtga ctgacatgcc tctgtcctgt 14160  
 tgcgagggcc tatagtcca agtgcattg ctctggggag ggcttcgtgg gtgcagagct 14220  
 gggcctgtgg agggccctca gacacaacac tgggtggggct cagagctcca ggggcactcg 14280  
 aggaagaca agaaccggct ctgagatgcg tgaatgtgac agtgcattg tagagatgga 14340  
 gaccttgtgg gtcccagaac caggactgca tatgactttc atatgtgggt atttttgcct 14400  
 tcattgggtcc ctctctgttt taaaaaaaat gtgtgattat gttgtcaca agagtttatt 14460  
 cctgtatatt gtgttaattt gtgttcagat ttgtaaagta aaattaaacc atttcagcca 14520  
 ggtgtggtga cacatgcctg tagccctagc tacttaccac agaggctgag gtgggaggat 14580  
 cgctgagcc cagaggttg aagctgcagt gagccatgat cacaccctg cactccagac 14640  
 tgggcgacag agctgagatc ctatttctgt ggccctaggt ccctgtgcct gctggaacag 14700  
 gacatcccta tcaccgtggg tggagccctt tgggtgtgta agacctatga atgagggaaa 14760

cttaggggtgc ccaagctgag gtagagccct cagaaccccc tgggatttgt attggagccc 14820  
 tcgtggcata acacaggtgg attatgcaat gggagtttct tacctataag caccacatg 14880  
 tgggcggtg gagggtagga gccatgcact agggcttcag cccccagccc cttcccgtt 14940  
 cagggcacac cttgcácttg gccagcctgg agctgggctt tcgggggtgg cacagcctgg 15000  
 gctggctctg gccagcataa tctgtttctc ttttgtccct ccagggagga cctcaggggt 15060  
 ggctgagctc ttacctggtt ttcaggcggg gccatagaa ggtacggggg gtggatcctg 15120  
 agttgggctt ctcgggagct cccatacatc acctactgct tctgactcta gttagtatcc 15180  
 ccttccccac taaaccctgc tcaactgtga ccctcacta acctggcctg actgtggctc 15240  
 tgaggcatct agtggctctg cgctgggcct aggctaggct gggctgagga gagcctgggg 15300  
 tgcaggccag ggctctgtga ctggcacctg cggtgctctt gaggggtgtg cgtctgggca 15360  
 gctggctctc tctttggtct gggggctgca gtctgtctcc ctctgtgcag gctgcctcgt 15420  
 tttctgcctt gtgttttttg cacctggggg agggccgtaa ctggggaatg gccgggatgg 15480  
 tagaatgggg agtgtgctgt gccagcctc tggcacaaaa aatccagcca gggctgcagg 15540  
 ttccttggtg agctttgcaa atcgtccccg acctcagtgc tggctccgca ccatgtaccc 15600  
 ctgctgtgcc gttagccctg ttcctccca ggctccggg ctcagggcct gttgtcttcc 15660  
 tgcagactgg ctcttcgtgg ttgtggtatg cctggctgcc ttcctcatct tcctcctcct 15720  
 gggcatctgc tggtgccagt gctgcccga cacttctgc tgctacgtca ggtgcccctg 15780  
 ctgcccagac aagtgtgct gccccgaggc ccgtaagtgt cccgctcatg gccaccctgg 15840  
 tttgggcaac atcctgcac caaggggaagg aggtggccat ccacctgcc ccaggacagt 15900  
 ggcgttggtc tggaggggtg gaatttagcc agtggggaga aagtaggctg aggagggctt 15960  
 gctgtttaga ttgtcgttta cttcctccaa cttttagttt atttttatth atgttgttct 16020  
 tttcttttgt aagtataatc catacacatg gtaaaaatgt ccaacagtac aagatactag 16080  
 tcacatggaa gtaaagccct ctaaaaaaac caaatcttgg ctaggcgcag tgattacgcc 16140  
 tgtaatccca gcactttggg aggccaagac gagtggatca cttgagggtca ggagttccag 16200  
 atcagcctgg ccaacatggg aaaaccctg tctctactaa aaatacaaaa attagctggg 16260  
 catggtggtg atcgctgta atcccagcta ctcaggagac tgaggcatga gaatcgctta 16320  
 aaccaagaa gtggagggtg cagtgagctg agatcacgcc actgcactcc agcctgggag 16380  
 acagagtgag actctgtctc aaaaaaaaaa gaaaaaaaaa tgtaagtga aaaagttaag 16440  
 aaaccaaaaa aggtttacaa cactacatga tttaagcaaa aaaaattttt tttgttttag 16500

agaaagggtc tcattctgtc atccaggcag tgcagtgcga tcatagctct ctgcagcctc 16560  
 aaactcccgg gttcaagcag tcctcccggc tcagcctctg gagcagctgg gactgtaggc 16620  
 acacaccacc atgcccagct aatTTTTtga tttttgtttt ttgtagagac ggggtctcag 16680  
 tatgttgccc agcctgatct caaactcctg gcctcaggtg atcctcccaa gtcagcctcc 16740  
 ccaaagtgtc gggattacag gcatgtgcca ccatgctggc caatTTTTta aaattttctg 16800  
 tagagacagg gtcttgctat gttgcccagg ctggtcttga actcttgacc tcaagtgatc 16860  
 ctgcctcagg ctcccaaagt gatgggatta caggcatgaa ctaccacacc tggccttaaa 16920  
 cttaaagcaaa tttttttttt tttttggaga cagtttctact ctgtcgccca ggctggagta 16980  
 aagtggcgtg atctctgtct actgcaacct ccgccccccg ggtttaagct attctcctgc 17040  
 ctgcagcctcc cgagtagctg ggatataggc gcctgccacc acgcctgact aatTTTTtga 17100  
 ttttttagtag agacgggggtt ttgccatgtt ggccaggctg gtctcgaact cctgacctca 17160  
 ggcagtccgc tccccgcac ccctaccttg gcctcccaaa gtgttaggac tacagggtgtg 17220  
 agccaccatg cctggccaaa tttaaagcaaa tgtttgaaaa cacataccca caggaatgct 17280  
 gcacatttta ccagctact atgtctaggg tcgtatctag cacaccagca tggctactgt 17340  
 ggagagctgg gactggatgt gagatgagag ctaaagggga agtaagcaaa ccaagcaggg 17400  
 gaaggtaaga gaagacagaa gacagagaga gagggacctt actctatgag aggagtcaga 17460  
 catgtgcaat tgaaaaagac ttgctcctgt ctctcttctg tgaatgtttg tgaatatccc 17520  
 aacgggacac tttcacagag gagctgattg acgtgggtcac agccatcagc cttgggacac 17580  
 cagaccacag tgtgtacact aagtggcact gatggacact tcagcatccc tctagctgct 17640  
 gtcccgtttc ccctcctcgg ggaccacagc tgttgccagt ccttggtttc cttcaggagg 17700  
 gtgtctgggt agaccagcct gtgtgcacac agtccaagat acatgaacag tgaagtgcc 17760  
 ggcaatcctt gcaagcatgg gcaggtggag agctgaggcc tgcttgacac cttcctgctc 17820  
 agaagcccag tgagcagttt ccctccctag ggctcagtgt catcccctat aaaatggggc 17880  
 ttatggcaga gctcaccaca ctgggtgcat ctggggattt ggcgagctca tgtgcacacc 17940  
 attgagcatg gggcccaacc tatataaaat attctacgtc tgtcagctgc tgggcactgc 18000  
 cactatcagc ctgagtagtg actgagggac agggcaccag tcagagccct ggtgcacaca 18060  
 gagtgacccc agagaagcag cttccctct ctgagtcctg tttccttctg ttaggtcctg 18120  
 acttcatggg ttgttggttag cattaaggaa gtcgctggct aatTTtatag tcattgaagt 18180

cagtgggtgtg caacctgggt cctcaaagga tcacttccct gaaaaaatc cactgctccc 18240  
tggaggctta tgcaggccat cccatcccct ccctcttggt gtgttcagct gacagctttt 18300  
tgctcagtga gtaagtgtta ggtccatttc acagatgggc tgcaaccaag tttgcagtga 18360  
accactaag accagagcta gggccaggac taaatgctgg tcccaatgcc acattcccct 18420  
gtccccacac cacatttcct ccatccggag accctgttac cccaaccag ggccccatta 18480  
actccctggc agaggccctg ttacatctgc tgctgccaca gcctccgcc acccttcagg 18540  
aggcagcagg tcccactgct gatgataaag ttgcaggctg cctgagctaa tgaaggggct 18600  
tcctctaggc tgtgcactta gtcttctgct tccaaaccaa atcagagggtg aggcaccctc 18660  
tctgggcca tctctctcct ccattttcct gttgggggtcc caggaggagaa gccacttgcc 18720  
tagggcccag gaattttgca agcctcttgc cctagggagg aaggaaggga ggaggatctt 18780  
accttgaact gtcaagccta gagcctgggtg gggcaggcag aaatgggtgc agtccatgag 18840  
ttagaaacac tagaggagac actttgctgc ttggccgggg caggcaagtt aattcccag 18900  
gctcctgcca ctgcatctca atctggaagg tgaccagggtg ggcaggacc acgtctccca 18960  
gatgactcat tttttctaga acaggggctt ggctgccaaa gaggatactt gatttcggct 19020  
tgtggggaca gtgggtggacc cagcatctgg gctttatata aagggcagct ttgttgccct 19080  
gtaaacacac agaccatggg tggccacttc ttccagtaag ttagctgggg agttggaagt 19140  
ttaggtaaaa ccttttgatt gacaaatgtt ggcgaattac catgctgtta aatgaaacat 19200  
tgttctgcca ccctggggct gtgggtgcct gcgtgcacc tctgaaaaat cacacaggaa 19260  
gtgggggtgg gtctctgtga agctgggtgc cccagcctc agggatgctg cagaaatgga 19320  
atgaggacca acagggactc agatgtccaa ggaagctcta cagcggagag gacggcttgg 19380  
gaaggaggtc caggcccagg tccctccgga acccaatggg tatggggcag cctggctcct 19440  
gcctcatccc ctttctcctg ttgattgtgt cctcacagt tatgccgcc gcaaagcagc 19500  
cacctcaggt gttcccagca tttatgcccc cagcacctat gccacctgt ctcccgcaa 19560  
gacccccccc ccaccagcta tgattcccat gggccctgcc tacaacgggt accctggagg 19620  
ataccctgga gacgttgaca ggagtagctc aggtgaggcc gggggaagca ggaacagctg 19680  
gtgggagtgt gctgggcata tggacactga ggggcagggg ctggaaggaa gagtgtcttg 19740  
ggagccgagg aggggctctg ctctgggtgc gcggccactg acagccactc tccccagct 19800  
ggtggccaag gctcctatgt acccctgctt cgggacacgg acagcagtgt ggcctctggt 19860  
gagaatccat cgtcccgaag ttggatgtgc ctgtaaggga gaggggtggg ccaggatcca 19920



tectcccaaa ccgaccacca cccccctgtc cctagaagtc cgcagtggct acaggattca	19980
ggccagccag caggacgact ccatgcgggt cctgtactac atggagaagg agctggccaa	20040
cttcgaccct tctcgacctg gcccccccag tggccgtgtg gagcggggta agcaggagcc	20100
ttgggggtctg agggctttta aggtgggggg gtgaaacatg tctccctgat acctgccgca	20160
gggactcttg gtgcaaacc tggaccccgg gctcctccag cagtcagtga cccccccctt	20220
ccctgcagcc atgagtgaag tcacctccct ccacgaggac gactggcgat ctgggccttc	20280
ccggggccct gccctcacc cgatccggga tgaggagtgg ggtggccact cccccggag	20340
tcccagggga tgggaccagg agcccgccag ggagcaggca ggcgggggct ggcgggccag	20400
gcggccccgg gcccgctccg tggacgccct ggacgacctc accccgccga gcaccgccga	20460
gtcagggagc aggtctcca cgagtaatgg tgggagaagc cgggcctaca tgcccccgcg	20520
gagccgcagc cgggacgacc tctatgacca agacgactcg agggacttcc cacgctcccg	20580
ggacccccac tacgacgact tcaggtctcg ggagcgccct cctgccgacc ccagggtcca	20640
ccaccaccgt acccgggacc ctccgggaaa cggctccagg tccggggacc tcccctatga	20700
tgggcggcta ctggaggagg ctgtgaggaa gaaggggtcg gaggagagga ggagaccca	20760
caaggaggag gaggaagagg cctactacc gcccgcgccg ccccgctact cggagaccga	20820
ctcgcaggcg tcccgagagc gcagggtcaa gaaggtgagg gccgcccctc ctggcgcca	20880
gaccgtccct gggccccag ccgggtccccg cggtcatac ccttctttct ttctcccttg	20940
cagaacttgg ccctgagtcg ggaaagtta gtcgtctgat ctgacgtttt ctacgtagct	21000
tttgtatttt tttttttaat ttgaaggaa actgatgaag ccctgccata cccctcccga	21060
gtctaataaa acgtataatc acaagctctg gagagaacca tttgttcggc cgcgcggggc	21120
gggggaccgg ggctgctccc gtatgcgtct gtaaagcgcc gcgtcccggg ggcaccggag	21180
tccggggccg ggaggaagag acccagcctg gcccgggccg cggccgcgcc gccggccgga	21240
gaacgtgcc cgcgcagccg ccgcccgcct gcgtgcgcgc cccggccccg cccaggcgtg	21300
cgcattgcgc ccggccctcc gccttcgcgc accgcaggct ggccgtccgg gacgcgcgcg	21360
cgtcctctc cccttcagc ccatcccccc cagccccca ccgacctact ttactgtctc	21420
caaactcggg cagcccacct ggcccccgac gacccagcc cctgcaccgg gtaccccgac	21480
gttccatcca gaccgcgtt tcaccagggc ggcgcgcggc gacctcgcgc cccgcggagc	21540
cccgggctcg cgcgcgccc cccgcccccg gagacagacc agcgcgcgcg ccccgggccg	21600

cctcccccca gcgcgcgtcc gccccggggc tcgcgcgcgc gccgcgcgcg ccgcgcgcgc 21660  
cgcgagctc aagtaaagga ggaaaaaaaa aagggggaaa aatagaaagc ggcggcggct 21720  
gcagcagcga tccgccgcgc gactgggcca agccgggcgc cggccgcgcg agccggcgat 21780  
ccagggcact ggcggcggcc agccagggcg ggccgtgttc aaaaaaaaaa gtcgcggcgc 21840  
cggcggtgc tcaggaagg aggcctgagg gccgcgtgca gcgggcgggc agctgggtgg 21900  
gctgggggcg gccgcgcgcg gtcccggagc ctggggccgc ccggagccgc cgggcgggcg 21960  
gaggcggagg cggcggcgcg tgcagcggct gcaggagcgc cggcggtgc ggcggcgcgc 22020  
gcggcatctc ctctcacat gacccactg tttgtccccg tgatcagcgc gagcggctcc 22080  
cgtatctct cctccccctc ctgcgcgcgc gcgtgagcgc cgggctcggg gcccccccg 22140  
ccgcgcgcgc cctccccctc ctccctcccc tccctcccc tcccccccg gccccgcgc 22200  
cccccgccc ccgcccccc catggacatg ctggaccgcg gtctggatcc cgctgcctcg 22260  
gccaccgctg ctgcgcgcgc caggtaagat ccccggccgc gccgtgcccc cgcgcccccg 22320  
ccccggcccc ggccccgcgc cctgcaggcc ggggcccga tgatcccag cggccgcggg 22380  
cccggctcaa aatggaggcc gccgggcgcg gggggacctg gcgcctcccg cccccggccc 22440  
ccggcctcgc cggcgcccc ggccctcaggc gcggccgggt gggactgggg ccctgcagct 22500  
gggcgcgggg gcgggggcgc gggcgcgggc cgcgctgacc ctgctccctc ctgtgcccct 22560  
ggcagccacg acaagggacc cgaggcggag gagggcgtcg agctgcagga aggtgagtgc 22620  
ttgccggggc ggccgcgcgc ggggagggt gggggcgctc ggcgcgccc tgaccgtgcc 22680  
ccgaccctcc tcggccccag gcggggacgc cccaggagcg gaggagcaga cagcgggtggc 22740  
catcaccagc gtccagcagg cggcggttcg cgaccacaac atccagtacc agttccgcac 22800  
agagacaaat ggaggacagg tgagcggcgc gccgcgagg cgaacgggcg ggcgggcggg 22860  
cgcgcgggga aggctcggac ctggccccag cgcgggcctc gccgctctgc cggccctgc 22920  
aggtgacata ccgcgtagtc cagggtgact atggtcagct ggacggccag ggcgac 22976

<210> 20

<211> 30

<212> DNA

<213> Rattus norvegicus

<400> 20

gttacagaat tcgccgcgat ggcgccggcg

30



<210> 21  
<211> 20  
<212> DNA  
<213> Rattus norvegicus

<400> 21  
gccaggacag tgtacgcact

20

<210> 22  
<211> 20  
<212> DNA  
<213> Ratus norvegicus

<400> 22  
acctcaggtg tcccgagcat

20

<210> 23  
<211> 20  
<212> DNA  
<213> Rattus norvegicus

<400> 23  
gaagatgact ggcgatcgag

20

<210> 24  
<211> 20  
<212> DNA  
<213> Rattus norvegicus

<400> 24  
acctctatga cccggacgat

20

<210> 25  
<211> 20  
<212> DNA  
<213> Rattus norvegicus

<400> 25  
caccaccctg acagtgcgta

20

<210> 26  
<211> 20  
<212> DNA  
<213> rattus norvegicus

<400> 26  
ctgggggcat agatgctcgg

20

<210> 27  
 <211> 20  
 <212> DNA  
 <213> Rattus norvegicus

<400> 27  
 gccctggaag gcctcgatcg 20

<210> 28  
 <211> 20  
 <212> DNA  
 <213> Rattus norvegicus

<400> 28  
 caagtcacctt ggatcgtccg 20

<210> 29  
 <211> 20  
 <212> PRT  
 <213> Rattus norvegicus

<220>

<221> Misc\_Feature  
 <222> 169..188  
 <223> Position in SEQID2

<400> 29  
 Ser Ala Gln Asp Leu Asp Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile  
 1 5 10 15

Val Leu Gly Arg  
 20

<210> 30  
 <211> 15  
 <212> PRT  
 <213> Rattus norvegicus

<220>

<221> Misc\_Feature  
 <222> 556..570  
 <223> Position in SEQID2

<400> 30  
 Glu Glu Gly Gln Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr  
 1 5 10 15

<210> 31  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 31  
atgcaacagg acggacttgg a

21

<210> 32  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 32  
tcagacgact aaactttccc gactcagg

28

<210> 33  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 33  
ctacaacccc tacgttgagt

20

<210> 34  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 34  
tcgtgacctg acctttgacc agac

24

<210> 35  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 35  
cctgagctac tcctgtcaac gtct

24

<210> 36  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 36  
aggccgagat cgccagtcgt

20

<210> 37  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 37  
ctacatggat ccagtcatgc cgaagat

27

<210> 38  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 38  
cgacaactcg agtcagttgg tatcatgg

28

<210> 39  
<211> 15  
<212> PRT  
<213> Homo sapiens

<220>

<221> Misc\_Feature  
<222> 1..14  
<223> Identical to 5 .. 18 in ref swissprot :Q07021

<400> 39  
Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val Ala Gly Tyr  
1                    5                    10                    15

<210> 40  
<211> 16  
<212> PRT  
<213> Homo sapiens

<220>

<221> Misc\_Feature  
<222> 2..15  
<223> Identical to 268 .. 282 in ref swissprot :Q07021

<400> 40  
Cys Tyr Ile Thr Phe Leu Glu Asp Leu Lys Ser Phe Val Lys Ser Gln  
1                    5                    10                    15

<210> 41  
 <211> 21721  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
  
 <221> exon  
 <222> 1898..2253  
  
 <221> exon  
 <222> 3438..3782  
  
 <221> exon  
 <222> 12064..12183  
  
 <221> exon  
 <222> 15049..15105  
  
 <221> exon  
 <222> 15670..15816  
  
 <221> exon  
 <222> 19486..19659  
  
 <221> exon  
 <222> 19806..19865  
  
 <221> exon  
 <222> 19963..20094  
  
 <221> exon  
 <222> 20236..20864  
  
 <221> exon  
 <222> 20954..21094  
  
 <221> Misc\_Feature  
 <222> 715  
 <223> diverging nucleotide, G in ref genbank:AC002128  
  
 <221> Misc\_Feature  
 <222> 1229  
 <223> diverging insertion, G in ref genbank:AC002128  
  
 <221> Misc\_Feature  
 <222> 3676  
 <223> diverging nucleotide, T in ref genbank:AC002128  
  
 <221> Misc\_Feature  
 <222> 5039  
 <223> diverging deletion, G in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 5118

<223> diverging nucleotide, C in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 7337  
 <223> diverging deletion, C in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 8294  
 <223> diverging nucleotide, G in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 8604  
 <223> diverging nucleotide, C in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 8928  
 <223> diverging nucleotide, A in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 9021  
 <223> diverging nucleotide, G in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 9851  
 <223> diverging insertion, GAATGAAA in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 9878  
 <223> diverging nucleotide, C in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 11478  
 <223> diverging nucleotide, T in ref genbank: AD000684  
  
 <221> Misc\_Feature  
 <222> 11577  
 <223> diverging deletion, C in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 11779  
 <223> diverging nucleotide, T in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 13411  
 <223> diverging deletion, T in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 13538  
 <223> diverging nucleotide, G in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 13896  
 <223> diverging nucleotide, G in ref genbank:AD000684  
  
 <221> Misc\_Feature  
 <222> 14912  
 <223> diverging nucleotide, A in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 16732  
 <223> diverging nucleotide, C in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 17169  
 <223> diverging nucleotide, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 18946  
 <223> diverging deletion, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 19474  
 <223> diverging nucleotide, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 20500  
 <223> diverging deletion, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 20501  
 <223> diverging deletion, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 20502  
 <223> diverging deletion, A in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 21270  
 <223> diverging nucleotide, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 21356  
 <223> diverging insertion, T in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 21476  
 <223> diverging nucleotide, A in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 21588  
 <223> diverging insertion, C in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 21601  
 <223> diverging deletion, T in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 21635  
 <223> diverging insertion, G in ref genbank:AD000684

<221> Misc\_Feature  
 <222> 19963..19965  
 <223> Potential variant splicing site AAG

<221> Misc\_Feature  
 <222> 1..21721  
 <223> n= a,g,c or t

<400> 41  
 aacagtttgg cagttcctca aaagggttaa aatagaacta ccaagtcacc cagcaattcc 60  
 attcttaggc atatattcaa aagaaatgaa agcagatatt tgtacaccag tggttcacagc 120  
 tgcactattht acaatagtca aaaggtagaa acaacctagg tccatccaca aatgaatgga 180  
 taaataaaac gtagcatata catacaatgg tacactagtc cgctgtaaaa agaaattttg 240  
 atcttactgc atgctacatg gcttcgacat actacaacat ggatggacct tgaaaacatt 300  
 attctttgtg aaataaacta gacacaggac aaatgttaga cgattccact tatatgaggc 360  
 acctagaatg ggcaatttgg taagcaaagt agaatagaaa ttactagggg cacaggtagc 420  
 agggaaatggg gagttactgt ttaatggtea cagagtttat gttggggatg atgaaacagt 480  
 ttcggggata aagagtgggt actggtacac gacattgtga atataactaa tgccactgaa 540  
 ttttacactt gaagtggta aagcgataaa tattatagnt ttgcatattht tatcataaaa 600  
 atatthttht aaacgatgaa gggacgtgaa cgggttgaaa ttttataaaa agtggccagg 660  
 gaagggtgta ctgcaatggg gtccacagg agggaggaaga tcatgtggac atctccggga 720  
 aggggtgttct ggcagaggga gtagcacggg cgatggctct gaggactgtg agaagtatag 780  
 ttggaaacag cgaggaggcc aggggtgtccg aagctgagta agccagagag agtgggagga 840  
 ggtgagataa gagggggaag gtcagtttct gctgagagtg agggaggacc acaggagggc 900  
 tgtgagcagg tggacgtgat ctggcttgag ttttaacagg gccagtagaa caaagcacgc 960  
 ctgggtaccg aaaccagcca ctggccagtt ggcaacctgg gggagtctaa cgcgaggaag 1020  
 cgcccagggt tccccagga tgcgctthtcc ctgcgcccca cctggagaca gcagagtcac 1080  
 gccagcgtc ggcagggctg atcgccgcgc cgcgcccccg ccctcggtcg cagggtggctc 1140  
 gttccgggaa ttcctaagcg gaaaccggtc ccaagccccg cgccttcgct cggccccctt 1200  
 aagagccaga atttccggag ggctgacccg gggctaggga tgcccagggg ccgaaccaca 1260  
 agttgggaac ggggtggggga ggtggcgaaa acttccgaag tggaattcca actthtctg 1320  
 gccctgattc cccttgggca tccctgangg ggcagagctt cccttccggg gactthtagag 1380  
 ggttcctcag gtcactaac tgggagacac agggaggccc aagcgcccc cctccacccg 1440  
 gtccggagga accccagtgg aagtggagaa gtcaggcgcc accaacaagc ctctcccagc 1500  
 caggactthg cttagactcg ctctcccgg cagggcgcac ctaggcgggt ccatcgccag 1560



ccgaggagag gggtttgggc agggagggaa caggtgcgcg gcgggacccg ccctatctca	1620
acaggtgaat cgctccaagt gggctctcgg tgcattggatc tcgggtgcgc tggtttggcc	1680
ggagcagatg ggggcccggaa gggacctgtg gtccgcaggc gccctcccag cgggccagtc	1740
acttggttcg ggccctgggg gacggagcgc acctgggtca gccacttcc ggggagggag	1800
gcagaggaac ccctccccgc cgctcaccac taagcccagc cctcggctcc cacccttgtg	1860
tacctgggccc gaaccattca ccggagcgcg cagcgggtgg agtgtggctc ggaggaccgc	1920
ggcgggtcaa gcacctttct ccccatatc tgaaagcatg ccctttgtcc acgtcgttta	1980
cgctcattaa aacttccaga atgcaacagg acggacttgg agtagggaca aggaacggaa	2040
gtgggaaggg gaggagcgtg caccctcct ggccttgggt gcgcgccgc cccctaaggt	2100
actttggaag ggacgcgcgg gccagacgcg cccagacggc cgcgatggcg ctggtggccg	2160
gcgggctctc cagagggctg ggctcccacc cggccgcgc aggcggggac gcggtcgtct	2220
tcgtgtggct tctgcttagc acctggtgca caggtacggg gcacggggcc tctgacgctg	2280
cggaaacgcc gagggaaact tagaggggga tggatggagt tggaggcggc gggaagcggg	2340
aagcgggggt ctcagaggct gggaccttcc gatcccttg gtcttgggcg atctgttgcg	2400
ncgcgggagt gagaggaatt cccatttgt gccggggagc gctccccgc cccttatctg	2460
gaagatagca ggaagtgaac ctccctggac ggtgagacc ggagcggcag ggagaatgga	2520
actctttgtg gggagggagt ggaagaccgc ccgatctctg ggaaaagaaa agccgggatg	2580
ggacttgggc gcacccgggg atttctaagt ttggagtaa cggggagagg gcacgggagg	2640
gctggatcag acgcttccta gagggacaga gacgaaggaa caatgcctag gcctcgggtg	2700
ggtgtgggac tggggactcc ccatcccccg caccacacc acctccgcg ggctccggat	2760
tatacgtgcg taagagtctg gtgggatgga ttacggact tgaaaccgac ttctgctggc	2820
aggctttcac ctggatggga tatttgggtg gtgatgaggt ctttcccag acacttttgg	2880
ttcagtcatt tgaaatgact ttagagtagg gtgaggtggg gggaggctga tggagatatt	2940
gtgggggctt tagtcctcc atggcaaagc agttcaggca acaactcca tggttttccc	3000
tccaaattca aaaggccccg ggtaacctgg aatccttcgt agtcggtttt gaagtggggc	3060
cttgggcgct gggggcatca acatggccat ctgggcttgc ctgcccaggc cacacagagg	3120
ccccttggtg tgggtgaatg gcaaagggaa gaggggactg gtgtggttca gaggccacag	3180
gctgggaaga gggatggcgg gcgagtccaa ggaaactggc cgtgtcaccg tgcacctgcc	3240
acttcagccc cacgggtcta taaaatgggc atgattatcg tggctacctc actggtcctg	3300

gcaattaagg aacaatgtgt gccaggcact ctgtaaacca catacttgcg agtgtcaagc	3360
tggtgacagg tggcgttcct gttgaagcac ctccctgagc tcacagcaac ccttgctgtc	3420
tctcctcttg ccctcagctc ctgccagggc catccagggtg accgtgtcca acccctacca	3480
cgtggtgatc ctcttcacgc ctgtgaccct gccctgtacc taccagatga cctcgacccc	3540
cacgcaaccc atcgtcatct ggaagtacaa gtctttctgc cgggaccgca tcgccgatgc	3600
cttctccccg gccagcgtcg acaaccagct caatgcccag ctggcagccg ggaacccagg	3660
ctacaacccc tacgtcgagt gccaggacag cgtgcgcacc gtcaggggtcg tggccaccaa	3720
gcagggcaac gctgtgaccc tgggagatta ctaccagggc cggaggatta ccatcaccgg	3780
aagtatgttg ggcagggcag ggggatgagg ctgggcttgc ccgggtggtg ggactggcgt	3840
ccttgctcgg gacctggagt ccccatctga aagctcttga gtgccagtgt ctgaaaggac	3900
cattgaaggg agcaattctt tttttttttt tttttgaaga tggagtcttg ctctggactc	3960
caggctggag tgcagtgggt cgatctcagc tcaactgcaac ctccacctcc caggttcaag	4020
caattctctt gcctcagcct cccgagtagc tgggactcca ggtgcgtgcc accacgcca	4080
gttaattttt gtatttttag tagagatggg gtttcacat gttggccagg ctgggtctca	4140
actcctgacc tcaaatagat tgcccgcctt ggcctcgcaa agtgctgaga gacaccatac	4200
ccagcctaaa gggagcgatt ctattctact attcttcctt ctgctaatac ttccattctt	4260
taatttaata acgaagattt tttgagtacc tgtcatatac cagggtgctgt tctgggccct	4320
gggaatacag ctgttaacaa aatcatcaaa ccacttcctt cgtggagccc acattgcagt	4380
gagagagaca aacacgacac acactctcaa gtccttgaag ataaagaaaa ctgggtaacg	4440
gagagaagag gccagggttt gttctataat cattaataac acgagcagta agaagtaaaa	4500
tttatctaag taacaactta taaagggtct actgtgtgct aagctctcat ccaggttccc	4560
aaggattaac tcagaccaca cagtaattga atagattcta tcattgtcat cttacagagg	4620
cccagagaga gaaagtgact tgcctagtgt catagctggg aacggggctg ggattctaac	4680
tcagccactt tgggtctagt ggccaagctc ctaatccctt tgcttgcta ggggtggtccg	4740
cagaggactc acagaggaga tggcaggagt gaactgcagg ggcaagagag cttaatggag	4800
aaagcctgtg acatgccagg aactgcacac atattctccc attgagtcct ctcccttacc	4860
ctcctgacag ctgaggcaca gagagggtac cttgttcaaa tgggtgcata ggaagtcaaa	4920
gtctggagct ggggtttgaa cccaggcagc cctgagaacc ttgttctttt tttttnann	4980

ggagtctcgc tctgtcgccc aggctggagt gcagtggcgg gatctcgget cactgcaagc	5040
tccgcctccc gggttcacgc cattctcctg cctcagcctc ccaagtagct gggactacag	5100
gcgcccgcga ctacgcctgg ctaatttttt gtatttttag tagagacggg gtttcaccgt	5160
tttagccggg atggtctcga tctcctgacc tcgtgatccg cccgcctcgg cctcccaaag	5220
tgctgggatt acaggcgtga gccaccgcgc ccggcccctt gttcttaact gtaatgctgc	5280
ctcctgatag gatgtgcctg ttgggactaa gtaaggggca gtcattcatt cattcatttg	5340
gtatttatca agcatcgact atgtgtcgtt ggtgctgggg atagagggtga ttgggatggc	5400
tgaagtttct gtcgtcaagg agatgacatt ctgggtggagt nagactggca gtaaatnaag	5460
cagataaaga aagagtatga gaatttcaaa gtctgggcac ggtggctcac gtctgtaatc	5520
tcagcacttt gggaggccaa ggtgggtgga tcacctgagg tcaggagttc cagaccagcc	5580
tggccaacat ggtgaaaccc cgtctctact aaaaatacaa agattagcca ggcatgggtg	5640
cacatgcctg taatcccagc tactcaggag gctgaggcat gagaatcgct tgaaccagc	5700
aggcagaggt tgcagtgagc tgagatcgca ccactgtact gcagnttggg cgacagagt	5760
agactctgtc tcaaaaaaaaa aaaaaaaaaa aaagactccg tcaaggtata agaatgtcag	5820
agagtactaa gtgttgcaaa gaaaataaca ccaggctggg tgcattggct catgcctgta	5880
aatttcagca ctttgggagg ccaaggcagg aggatcactt gagcctagga gtttgagacc	5940
agcctggaca acaaaatgag accccatgtc taaaaaatt ttaaaaattt aaaaattagc	6000
tgggcatggt ggcattgtgc tgtggtccc gctgctcagg aggctgaggt gggaggattg	6060
cttgggcttg agaggtcaag gcttcagtga gtcattgatc tgccactgca ttccagcctg	6120
ggtgacagag tgagaccctg tcttgaaatg aaaagaaaat aggctgggcg cagtggctca	6180
cacctgtaat ccagcactt tgggaggccg aggtgggtgg atcacctgag gtcaggagat	6240
cgagaccagc ctggccaaca tgggtgaaatc ccatctctac taaaaataca aaatttagcc	6300
gggcgtggtg gtgggcgcct gtaatcccag ctactcggga ggctgaggca ggagaatcgc	6360
ttgaacctgg gaggcgaagg ttgcggtgcg ccaagattgc gccactgcac tctagcctgg	6420
gaaacagtga gactccgtct taaaaaaaa agaaaaaaga aaatagcact gggatgatgtg	6480
ctacatggaa tgacttgggc tgtgaatatg atttgaggag ggcctgggcc tgggccttac	6540
agaacctaga aggagagag gaaggggagg ggcagggtgc cagggatgaa ggctcacgta	6600
cctcatgtct tagtgtgtgt tcaactgtctt aaacaagaat ttaaagttag gcatggggca	6660
gagcggggaa gggagcatcc ctttgcagac cccaagaagc cagggaactgg agcacattct	6720

gctagaggat cgatgggaag caggggtcca ggggctgagc ctatgtcagt cctgtttcag	6780
aggaggcacc aggcttgctt gccctgaatt tctgtgggca gctcagccat gagcatccta	6840
ctgttattga ggtcacaggg ctgcttaggc cccctcctct ctaaccacagg gattgtgcct	6900
gcctggacca ggcgtgactg ctaagcttct gccaggacaa gccaaatact gagggtgctt	6960
cctctgctgg acgcaaaagt ccaggatgac ccccaggct ctgtctcggg gaaggggccc	7020
tgcattgctcc aggggcctca caggcctggg tctttcaaac cacccccacc tgggcctgtg	7080
tttgatcaag gccctgagtg taaacatcca ttgtgtgtgt cctttcagga aatcccatag	7140
ccataggagc ttctctgttt tcagctttga ggatggggaa aagtggactc cccgtggtgt	7200
tcctagggtc acccactgtg ctgggggtttt tctgttgnnt gttgtttttt ttctgttgcc	7260
caggctggag tgcagtgggtg caatctcagc tcaactgcaac ctctgcctcg caagttcaag	7320
tgattctccc gcctcagcct cctgagtagc tgggattaca ggtgcacacc accacacctg	7380
gctaattttt gtatcttttt ggtagagatg ggatttcgcc atgttggcca ggctggtctc	7440
aaactcctga cctcaggtga tctgcctgcc ttggcctccc aaagttctgg gattacagat	7500
gtgagccacc atgcccggcc tatcctgggt tcaaaagtga aaatagtcct ggataaggta	7560
gaaggctgtc cactccaggc atccctccgg tccgggtggct cattccctgc tttgtccttc	7620
catgcttttg gtgatggacc agcacctgga caggaggccc tgttccacct cctcgggctc	7680
cttgggggtcc aagtgcccc acctccagct gcactgcagc agagagccca tgggacctct	7740
gaaatcatga aggtcacctt tgcggtgtat aaagaaggaa ccagagggtg gagatgtgga	7800
ggaggcctgg ctgctgttcc cactggagac ctggcatctt ctccccgacc taaaacaatg	7860
aaagcagtgc tcagcccgga tgagatcacg gccagcccaa gaccaggaac agggtaggcc	7920
ctgcaggaag aaggtgtgcc cagaccttag gatggatcaa aagaagccgg aaaactatat	7980
tttttgtgag ttttgaaaat gtcagacagg tcaaacaaaa cacagtgagg tccagcctcg	8040
gcctacaaga tgccagattt caaccctgg cctatatgat ctgtttgcca tggcaggcgg	8100
ttctgtcca cctcttttgt ttatagcagg gaccagctct tgagctccag tgttgaagag	8160
gcacggtcag ggtctgatct gaagacactg gtggctcatg cctgtaatcc cagcacttca	8220
ggaggccgag gcaggaggat tgcttgagga caggagctgg gagaccagcc tgggcaacac	8280
agtgagaccc agacactaca aaaaaataaa tttagcgggg catgatggca caccctgcta	8340
ctctggagat gggaagattg cttgagccta ggagttcgaa gctgcagtga cccatgatcg	8400

caccactgca ctccagcctg ggcgaccaag ctaggccctc tcaaaaaaga tacagggtgga	8460
aaaatgatgg acgaagaggg cattgtggca aacctgggga tttaggagaa cctagtttgg	8520
aattctatga ggattcaatg aaagaatgtg tgtagagggg cccagcacat agtaagagct	8580
caataaacgg tgggggctag ggggtgggtgc tcatgcctgt aatcccagca ctttgggagg	8640
ctgaggcagg tggatcactt gagccctgga gttcaagatc aacctggaca acaaagcaag	8700
atcccatctc aaaattaaaa aacaacacca acaacaaaaa aacagtggct tagatgcctg	8760
atcattaggg taagtcgtgt cctcaacccc ttcacatctg ctctgaaggc caccatatcc	8820
ggaagccttc cctggcctcc ttgtttaaaa tggcacagcc cccactccac gcctggcact	8880
ctctgctgtc cctgattcgt tttctccata cagcttatct ttgtctggta tgtgacatag	8940
ttaacatttt atatttgtct ttctttccta gttagaatct gaactctaga agggcaaggg	9000
caaggattta taactcaaag attccgggct taggcctctt ttatatctt gattttgagg	9060
ttaattaaga gctcaggcct agcgagggtg ctcatgcctg gaatcccagc actttgggag	9120
gccagggcgg gcagatcact tgagggtcagg agttccagac ctgcctggcc aacacagtga	9180
aaaacctgtc tctactaaaa atacaaaaat tagccagtta tgttggcagg cgcctataat	9240
cccagctact caagaggctg aggcaggaga atcgcttgaa cccaggaggc agaggctgca	9300
gtgagccaag atcgtgccac tgcactccag cctgggcaac agagcgagac tccatctcaa	9360
aaaaaaaaaa aaaattaaga gctcaaagag ttgttttca taggcagcag aatgagaaaa	9420
gtttacaaaa tagtttaaata gacaataaag tcattataga ttaacataaa taaaatacct	9480
tttatgaaaa aaataatcat tttctgaaat cagacaaaac attgtgaatg agaagggtggc	9540
atggttttat ttttttgcaa gtctccgaag cctggctgga tagaagagcc tggcttctca	9600
gagctgcttc agtctgttgt gatattctatt gtatgtcacg tagcctctgg aaaactccac	9660
agttagtatt gttgggaaaa taactttgac ctcaggatct cctgaaaacg tcttggggaa	9720
ccccagggtc tagaggctgc agtttgagaa ctgttgctgt ggtatcccag gtgtctcaaa	9780
tactgcctag aacatagggtg gtactcagta attattgttg naaggatgaa tgaatgaatg	9840
aatgaatgaa tgaaagaaag aatgtgtct ttgaatctag ccatgtgcc agaatgatga	9900
gacagatgac aaaagctaag ggactttagc atgaggagag ggggttcgtt tccttttttt	9960
tctttttttt ttgagatgga gtctcactct actgcccagg ctagagtgca gtgggtgcaat	10020
ctcagctcac tgcaatctct gcctcctgag ttcaagcaat tctcctgcct cagcctccag	10080
ggtagctggg actacagggtg cgtgccacca tgccatagcta attttttaca tttttggtag	10140

agatgggggtt ttaccatggt ggccgggctg gtctggaact cctgacctca agtgatccac	10200
ctgcctcagc ctcccaaagt gttaggatta cagggtgtgag ccaccatgtc cggccaagag	10260
ggtgttcatt tctgctcctt gccaggtatt gtgtcaggca ctggggaccc agcagtggct	10320
gagacagaca gggctctgcc tcacggagcc cacattttca ccaggcaaag gatggtcggc	10380
ccctaagctg ggagataaga cttcagcagt tgggtggggg agccgtggga gaagcccagc	10440
ccacaggggg acagtgcaaa tctagaacca aggcgatggc aggggtgagg ctggcacggc	10500
agctagagac cacgtcgtgc caagggcctt ggggacctg ggactatggg accttaggga	10560
aggcgtctgg aatgctgtag ccagacactg ttgcaaggag gatttttctg tagacatgag	10620
gccttcctta tgaagaaagc aagggttctt tcattcctgg gggtgccagg tgctgtggac	10680
tgcagcacgc gtggttgctg ccgtcacaga gctgtcatgc aggagggcag cgcgtccttg	10740
ggaaggtggc aggcaggtca ggctaggagg aaagaggccg ggaagctgag ggcatttcct	10800
gcccagatg cccaatgtag cctacttctg tccccagtgg cttaggcag agttgcctgg	10860
taggtgccct ggtcccaccc tggtgaaagg ctgaaggtat ttaattagt cctgagaagc	10920
agagaggaaa caggatgtgc caaaacactt tgatggatgg tagagttaac aggctccttg	10980
cctgcagctg cttcagacaa gagcgtcccc aagccctggg cctgacctgg aatgtgggga	11040
tggaagggga gggggaggaa ccaaggcact gggagggtaa gtctctctct cccacataga	11100
cacaccact ccttatgggt gcctgggcat ctctggtac ctagaatctg gcctgtttat	11160
ctccacaccc atccctgggg tctacactag gccctgtggg tggcagttca catcagggga	11220
gttctgactt tggctctgag aggtggttca gagatggctg taagttgaga agcacagact	11280
gctgggtgtg gtggttcacg cctgtaatcc cagcactttg ggaggctgag gtgggggtgg	11340
atcacctgag gtctggagtt caaaaccaac ttggtcaaca tggcgaaact ccatctctac	11400
taaaaatgca aaaattagcc aggtgtggtg gcagggtgcct ataatcccag ctacatggga	11460
ggctgaggca ggagaatcgc ttgaatctgg gaggcgaaga ttgtagtgag ccgagattag	11520
ttcgcaccat tgcatgccag cctgggcaac aagagtgaaa ctccgattca aacaaacaaa	11580
aaaaaaaaagc tgggcatggt ggagtgcctg tagtcctaac tactcaggtg ggaggattgc	11640
ttgagtccag gaggttgaag ttgcagtggg ctataattac accactgcac tccagccagg	11700
gccacagagt gagaccctgt ctctaaagaa agaaaaaaaa aaacaacctc aggctccgag	11760
ggcaccatta ctgctctaca ctgaagagct gtgcagcttt tccagacctg aaatgtcatc	11820



cacaaaacag aagtgataat ggtcctgcct cacagacttc ttgcagtagt ccaggtgttt 11880  
agaacggggt gtaaaaggcc gtgtgccctt ggtaggaatc ttngcatatg catttgatca 11940  
tctgcagcct gccagccca ctgcttgccc cctcctgggt gtgctgggaa ggggtctttg 12000  
gccctccagg ggtaggtgc ccagcctcc aaggtgccct cacgcctttt catcccgact 12060  
cagatgctga cctgacctt gaccagacgg cgtgggggga cagtgggtgtg tattactgct 12120  
ccgtgggtctc agcccaggac ctccaggga acaatgaggc ctacgcagag ctcatcgtcc 12180  
ttggtgagtg ggctgggaa gggggaggca tggcccttcc ttttgtccgc ttctgttctg 12240  
tctgccctcc cctgtgtccg ccctctgccc tccagcttac cctctgggct ctgtcgctg 12300  
ctctgctctc ccccaggctc tgccagtcac ttaggtccc ctgtgccctg caccacaggc 12360  
agggaccact ggcccacagt gcctccaatc acccaagcca aactaagaga agagtggaga 12420  
caattggaga ctctgccttt tcaaagtctc atttttaaaa aaaatccaga cttgggggtcc 12480  
gggtgcggta gttcatgcct gtaatcccag cactttggga ggccgaggcg ggtggatcac 12540  
ttgaggccag gagttcgaga ctagcctggc caacgtggca aaatcccgtc tctataaaaa 12600  
atataaaagc caggcgtggg ggtgcacatg cctgtaatcc cagttactca gaaggctgag 12660  
gcatgaggat tgcttgaacc tgggaggcag aggatgcagt aagccaagat caagccactg 12720  
cactccagcc tgggcgacag agtgagactc tgtccaaaaa aaaaaaaaaat ccagacgtgg 12780  
tcagagtcca tgggcagtga atgaggacag ttgatgggtg gcaaaatcga cccacctctt 12840  
gctacatccc caaggcctca tctcaccga gtccctcgcc aaagcacagc ggttttgccg 12900  
tgtgccctgc tgggatggcg ctgcatggca cacacactgt gtaagtttga gtgcagctga 12960  
aacgaagccg attccagaca cccaggggca gggcggggtg tccgtgtggc tgggaggcct 13020  
ccttgtgtta gggggatgtt gccatcgcc aggtgccctg ctgtaagcca acacatggag 13080  
tcttgtatga catgtgctct gcatgagtga tgccgctggg ctgtacactg ccatcttcac 13140  
atgtgtgaat gagcacgtga ctggggggta cttgggctgc aagacagagt tcatgtgtgg 13200  
gggatggaac acgtgcacca gtgaccagc aacctctgcc tgttcttcgg taaaatgcac 13260  
catttgcac agcagttccc aaaattagtc tccaggtcta ttacactct aaaacattat 13320  
cgagggtctc caagagcttt tgtttgtttc tgtgggtttt atgtctatct gttgcttaac 13380  
atattaggaa ttaaaatggg gagattttcc tttttttttt tttttttttg agatggagtc 13440  
tcgttctgtc gccaggctg gagtgcagt gctcgatctc ggctcactgc aagcttcacc 13500  
tcctgggttc acgccattct cctgcctcag cctcccaagt agctgggact acaggcaccc 13560

gccaccacac ccggctaatt ttttttgtat ttttagtaga gactggggtt caccatgtta 13620  
gccaggatgg tctcgatctc ctgacctcgt gatccacca cctgggcctc ccaaagtgt 13680  
gggattacag gcatgagcca ctgcccggcc ttaaaatggg gagatttttc aagcccaaga 13740  
tacacaagga agactgggca acatggcaag accctgactc tacaaaaaat tttaaaatta 13800  
accaggcatg gtggcatgca cctgtgagcc cagcttcttg ggaggctgag gcaggagtat 13860  
cgcttgcacc caggaggtca aggctgcagt gagccatgac tatgctactg cactctagca 13920  
tgagtgcag agaccctggc tcaagaaann canacaaaca cacacacaca cacacacag 13980  
catatagtcc attaggtatc agggcgatga tggcatcagg gagcctggga aactctactg 14040  
gacattcatg ggagaacaag tgaaaaaggc aaataacatc ttagtgttat tctaaaattt 14100  
cttcttttgg ccttgtggac aggaccacgc tttgagagct gtgactgaca tgcctctgtc 14160  
ctgttgcgag ggcctatagt gccaagtgc tgagctctgg ggagggttc gtgggtgcag 14220  
agctgggcct gtggaggccc ctcagacaca aactgggtgg ggctcagagc tccaggggca 14280  
ctcgaggga gacaagaacc ggctctgaga tgcgtgaatg tgacagtgc tgagtagaga 14340  
tgagacctt gtgggtccca gaaccaggac tgcatatgac tttcatatgt gggatatttt 14400  
gccttcatgg gtcccttctt gttttaaaaa aaatgtgtga ttatgttgtc acaaagagtt 14460  
tattcctgta tattgtgtta atttgtgttc agatttgtaa agtaaaatta aaccatttca 14520  
gccaggtgtg gtgacacatg cctgtagccc tagctactta cccagaggc tgagggtgga 14580  
ggatcgctg agcccacgag gttgaagctg cagtgcagca tgatcacacc cctgcactcc 14640  
agactgggcg acagagctga gatcctatct cgtgggccct aggtccctgt gcctgctgga 14700  
acaggacatc cctatcaccg tggttggagc cttttggggg gctaagacct atgaatgagg 14760  
gaaacttagg gtgccaagc tgaggtagag ccctcagaac cccctgggat ttgtattgga 14820  
gcctcgtgg cataacacag gtggattatg caatgggagt ttcttaccta taagcaccca 14880  
catgtgggcg ggtggagggt aggagccatg cgctagggct tcagcccca gcccttccc 14940  
gcttcagggc acacctgca cttggccagc ctggagctgg gctttcgggg gtggcacagc 15000  
ctgggctggc tctggccagc ataatctgtt tctcttttgt ccctccaggg aggacctcag 15060  
gggtggctga gctcttacct ggttttcagg cggggcccat agaaggtacg gggggtggat 15120  
cctgagttgg gcttctcggg agctcccata catcacctac tgcttctgac tctagttagt 15180  
atccccttcc ccactaaacc ctgctcactg tggaccctc actaacctgg cctgactgtg 15240



gctctgaggc atctagtggg ctggcgctgg gcctaggcta ggctgggctg aggagagcct 15300  
ggggtgcagg ccagggtctt gtgactggca cctgcggtgc tcttgagggt gtggcgctctg 15360  
ggcagctggc tctctctttg gtctgggggc tgcagtctgt ctccctctgt gcaggctgcc 15420  
tcgttttctg ccttgtgttt tttgcacctg ggggagggcc gtaactgggg aatggccggg 15480  
atggtagaat ggggagtgtg ctgtgcccag cctctggcac aaaaaatcca gccagggtg 15540  
caggttcctt ggtgagcttt gcaaacgctc cccgacctca gtgctggctc cgcaccatgt 15600  
accctgctg tgccgttagc cctgttcctt cccaggcctc cgggctcagg gcctgttgtc 15660  
tttctgcaga ctggctcttc gtggttgtgg tatgcctggc tgccttcctc atcttcctcc 15720  
tcctgggcat ctgctgggtg cagtgtgcc cgcacacttg ctgctgctac gtcagggtgcc 15780  
cctgctgcc agacaagtgc tgctgccccg agggccgtaa gtgtcccgt catggccacc 15840  
ctggtttggg caacatcctg catccaaggg aaggagggtg ccatccacct gccccagga 15900  
cagtggcggt ggtctggagg gtgtgaattt agccagtggg gagaaagtag gctgaggagg 15960  
gtctgctgtt tagattgtcg tttacttctt ccaactttta gtttattttt atttatgttg 16020  
ttcttttctt ttgtaagtat aatccataca catggtaaaa atgtccaaca gtacaagata 16080  
ctagtcacat ggaagtaaag ccctctaaaa aaaccaaatac ttggctaggc gcagtgatta 16140  
cgcctgtaat cccagcactt tgggaggcca agacgagtgg atcacttgag gtcaggagtt 16200  
ccagatcagc ctggccaaca tggtaaaacc cagttctcta ctaaaaatac aaaaattagc 16260  
tgggcatggt ggtgatcgcc tgtaatccca gctactcagg agactgaggc atgagaatcg 16320  
cttaaaccga agaagtggag gttgcagtga gctgagatca cgccactgca ctccagcctg 16380  
ggcgacagag tgagactctg tctcaaaaaa aaaagaaaaa aaaatgttaa gtgaaaaagt 16440  
taagaaacca aacaagggtt acaacactac atgatttaag caaaaaaat tttttttgtt 16500  
ttagagaaag ggtctcattc tgtcatccag gcagtgcagt gcgatcatag ctctctgcag 16560  
cctcaaactc ccgggttcaa gcagtcctcc cgcctcagcc tctggagcag ctgggactgt 16620  
aggcacacac caccatgccc agctaatttt ttgatttttg tttttttag agacggggtc 16680  
tcagtatgtt gccagcctg atctcaaact cctggcctca ggtgatcctc cgaagtcagc 16740  
ctccccaaag tgctgggatt acaggcatgt gccaccatgc tggccaattt ttaaaaattt 16800  
tctgtagaga cagggtcttg ctatgttgcc caggctggtc ttgaactctt gacctcaagt 16860  
gatcctgcct caggctccca aagtgatggg attacaggca tgaactacca cacctggcct 16920  
taaacttaag caaatTTTTT ttttttttg gagacagttt cactctgtcg cccaggctgg 16980

agtaaagtgg cgtgatctct gctcactgca acctccgccc cccgggttta agctattctc 17040  
 ctgcctcagc ctcccgagta gctgggatat aggcgcctgc caccacgcct gactaatttt 17100  
 tgtattttta gtagagacgg ggttttgcca tgttggccag gctggtctcg aactcctgac 17160  
 ctcaggcaat ccgctcccc gcacccctac cttggcctcc caaagtgtta ggactacagg 17220  
 tgtgagccac catgcctggc caaatttaag caaatgtttg aaaacacata cccacaggaa 17280  
 tgctgcacat ttaccacagc tactatgtct agggtcgtat ctagcacacc agcatggcta 17340  
 ctgtggagag ctgggactgg atgtgagatg agagctaaag gggagtaag caaaccaagc 17400  
 aggggaaggt aagagaagac agaagacaga gagagaggga cctaactcta tgagaggagt 17460  
 cagacatgtg caattgaaaa agacttgctc ctgtctctct tctgtgaatg tttgtgaata 17520  
 tcccaacggg acactttcac agaggagctg attgacgtgg tcacagccat cagccttggg 17580  
 acaccagacc acagtgtgta cactaagtgg cactgatgga cacttcagca tccctctagc 17640  
 tgctgtcccg tttccctcc tcggggacca cagctgttgc cagtccttgg tttccttcag 17700  
 gaggtgtct gggtagacca gcctgtgtgc acacagtcca agatacatga acagtgaagt 17760  
 gccaggcaat ccttgcaagc atgggcaggt ggagagctga ggctgcttg acaccttcct 17820  
 gctcagaagc ccagtgagca gtttccctcc ctagggctca gtgtcatccc ctataaaatg 17880  
 gggcttatgg cagagctcac cacactgggt gcctctgggg atttggcgag ctcatgtgca 17940  
 caccattgag catggggccc aacctatata aaatattcta cgtctgtcag ctgctgggca 18000  
 ctgccactat cagcctcagt agtgactgag ggacagggca ccagtcagag ccctggtgca 18060  
 cacagagtga cccagagaa gcagccttcc ctctctgagt cctgtttcct tctgttaggt 18120  
 cctgacttca tgggttggtg ttagcattaa ggaagtcgct ggctaatttt atagtcattg 18180  
 aagtcagtgg tgtgcaacct ggttcctcaa aggatcactt ccctgaaaaa attccactgc 18240  
 tccctggagg cttatgcagg ccatcccatc ccctccctct tgttggtggtc agctgacagc 18300  
 tttttgctca gtgagtaagt gttagggtcca ttccacagat gggctgcaac caagtttgca 18360  
 gtgaaccac taagaccaga gctagggcca ggactaaatg ctgggtccca tgccacattc 18420  
 ccctgtcccc acaccacatt tctccatcc ggagaccctg ttacccaac ccaggggccc 18480  
 attaactccc tggcagaggc cctgttacat ctgctgctgc cacagcctcc gccaccctt 18540  
 caggaggcag caggtccac tgctgatgat aaagttgcag gctgcctgag ctaatgaagg 18600  
 ggcttcctct aggtgtgca cttagtcttc tgcttccaaa ccaaatcaga ggtgaggcac 18660

cctctctggg cccatctctc tcctccattt tcctgttggg gtcccaggga ggaagccact 18720  
tgcctagggc ccaggaattt tgcaagcctc ttgccctagg gaggaaggaa gggaggagga 18780  
tcttaccttg aactgtcaag cctagagcct ggtggggcag gcagaaatgg gtgcagtcca 18840  
tgagttagaa aactagagg agacactttg ctgcttggn cggggcaggc aagnttaatt 18900  
cccgaggctc ctgccactgc atctcaatct ggaagggtgac caggtggggc aggaccacg 18960  
tctcccagat gactcatttt ttctagaaca ggggcttggc tgccaaagag gatacttgat 19020  
ttcggcttgt ggggacagtg gtggaccacg catctgggct ttatataaag ggcagctttg 19080  
ttgccctgta aacacacaga ccatgggtgg ccacttcttc cagtaagtta gctggggagt 19140  
tggaagttta ggtaaaacct tttgattgac aaatgttggc gaattaccat gctgttaaata 19200  
gaaacattgt tctgccaccc tggggctgtg ggtgcctgcg tgcaccctct gaaaaatcac 19260  
acaggaagtg ggggtggggc tctgtgaagc tgggtgtccc cagcctcagg gatgctgcag 19320  
aaatggaatg aggaccaaca gggactcaga tgtccaagga agctctacag cggagaggac 19380  
ggcttgggaa ggaggtccag gcccagggtcc ctccggaacc caatgggtat ggggcagcct 19440  
ggctcctgcc tcatccccct tctcctgttg attatgtcct cacagtgtat gccgccggca 19500  
aagcagccac ctgaggtgtt cccagcattt atgccccag cacctatgcc cacctgtctc 19560  
ccgccaagac cccacccccca ccagctatga ttcccatggg ccctgcctac aacgggtacc 19620  
ctggaggata ccctggagac gttgacagga gtagctcagg tgaggccggg ggaagcagga 19680  
acagctggtg ggagtgtgct gggcatctgg aactgaggg gcaggggctg gaaggaagag 19740  
tgtcttggga gccgaggagg ggctctgctc ctggtgcgcg gccactgaca gccactctcc 19800  
cccagctggt ggccaaggct cctatgtacc cctgcttcgg gacacggaca gcagtgtggc 19860  
ctctggtgag aatccatcgt cccgaagtgt gatgtgcctg taaggagag ggggtggcca 19920  
ggatccatcc tcccaaaccg accaccaccc ccctgtccct agaagtccgc agtggctaca 19980  
ggattcaggc cagccagcag gacgactcca tgcgggtcct gtactacatg gagaaggagc 20040  
tggccaactt cgacccttct cgacctggcc cccccagtgg ccgtgtggag cggggtaagc 20100  
aggagccttg ggtctgagg gcttttaagg tgggggggtg aaacatgtct ccctgatacc 20160  
tgccgcaggg actcttgggt caaacctgg accccgggct cctccagcag tcagtgcac 20220  
ccccctccc tgcagccatg agtgaagtca cctccctcca cgaggacgac tggcgatctc 20280  
ggccttccc gggccctgcc ctacccccga tccgggatga ggagtggggg ggccactccc 20340  
cccgaggtcc caggggatgg gaccaggagc ccgccaggga gcaggcaggc gggggctggc 20400

gggccaggcg gccccggggc cgctccgtgg acgccctgga cgacctcacc ccgccgagca 20460  
 ccgccgagtc agggagcagg tctcccacga gtaatggtgg gaggagaagc cgggcctaca 20520  
 tgcccccgcg gagccgcagc cgggacgacc tctatgacca agacgactcg agggacttcc 20580  
 cacgtcccg ggacccccac tacgacgact tcaggtctcg ggagcgccct cctgccgacc 20640  
 ccaggtecca ccaccaccgt acccgggacc ctcgggacaa cggctccagg tccggggacc 20700  
 tcccctatga tgggcggcta ctggaggagg ctgtgaggaa gaaggggtcg gaggagagga 20760  
 ggagaccca caaggaggag gaggaagagg cctactacc gccgcgccg ccccgact 20820  
 cggagaccga ctgcaggcg tcccagagac gcaggctcaa gaaggtgagg gccgccctcc 20880  
 ctggcgcca gaccgtccct gggccccag ccgggtcccg cggctcatac ccttctttct 20940  
 ttctcccttg cagaacttg ccctgagtcg ggaaagtta gtcgtctgat ctgacgtttt 21000  
 ctacgtagct tttgtatatt tttttttaat ttgaaggaa actgatgaag ccctgccata 21060  
 cccctccga gtctaataaa acgtataatc acaagctctg gagagaacca tttgttcggc 21120  
 cgcgcggggc gggggaccgg ggctgctccc gtatgcgtct gtaaagcgcc gcgtcccggg 21180  
 ggcaccgga tccggggccg ggaggaagag accagcctg gcccggccg cgcccgcgcc 21240  
 gccggccgga gaacgtgccc cgcgacgcca ccgccgcct gcgtgcgcgc ccgggccccg 21300  
 cccaggcgtg cgcattgcgc ccggccctcc gccttcgcgc accgcaggct ggccgcccgg 21360  
 agcgcgcgcg cgctcctctc cccttcagc ccatacccc cagccccca ccgacctact 21420  
 ttactgtctc caaactcggg cagcccacct ggccccgac gacccagcc cctgctccgg 21480  
 gtaccccgac gttccatcca gaccgcggt tcaccagggc ggcgcgcggc gacctcgcg 21540  
 cccgcggagc cccgggctcg cgcgcgccc cccgcccccg gagacagaca gcgcgcgcgc 21600  
 tcccgggccc cctccccca gcgcgcgtcc gcccgggct cgcgccgccc ccgccgccc 21660  
 cgccgcgcgc gcgcagctca agtaaaggag gaaaaaaaaa agggggaaaa atagaaagcg 21720  
 g 21721